

GanCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:41:05 ; Search time 18 Seconds
(without alignments)
1310.432 Million cell updates/sec

Title: US-09-846-512-2
Perfect score: 2443
Sequence: 1 MGENDPVAEAPPERSLFG.....TRVTSFLDTHEQMERDLKTT 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext C.5

Searched: 141601 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

141680.

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SwissProt_42.4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2432.5	99.6	454	1	TMS3_HUMAN	P5727 homo sapien
2	2226	91.1	453	1	TMS3_MOUSE	Q81100 mus musculus
3	882	36.1	492	1	TMS2_HUMAN	Q15393 homo sapien
4	875	35.8	490	1	TMS2_MOUSE	Q911QB mus musculus
5	695.5	28.5	455	1	TMS5_MOUSE	Q91040 mus musculus
6	689.5	28.2	457	1	TMS5_HUMAN	Q91363 homo sapien
7	677	27.7	435	1	TMS4_MOUSE	Q82655 mus musculus
8	674	27.6	417	1	HPS5_HUMAN	P05181 homo sapien
9	659.5	27.4	1035	1	ENTK_BOVIN	P90072 bos taurus
10	664.5	27.2	1019	1	ENTK_HUMAN	P90073 homo sapien
11	663.5	27.2	1034	1	ENTK_PIG	P90074 sus scrofa
12	659.5	27.0	436	1	HPS5_MOUSE	Q34153 mus musculus
13	658	26.9	437	1	TMS4_HUMAN	Q91rs4 homo sapien
14	654.5	26.8	416	1	HPS5_RAT	Q05511 rattus norvegicus
15	651	26.6	1069	1	KAL1_MOUSE	P91435 mus musculus
16	579.5	23.7	638	1	KAL1 RAT	P21272 rattus norvegicus
17	578.5	23.7	811	1	TMS2_MOUSE	Q9abio mus musculus
18	571	23.4	418	1	HATT_HUMAN	Q6235 homo sapien
19	570.5	23.4	638	1	KAL1_MOUSE	P26262 mus musculus
20	560	22.9	811	1	TMS2_HUMAN	Q81u80 homo sapien
21	549.5	22.5	638	1	KAL1_HUMAN	P0952 homo sapien
22	543.5	22.2	416	1	NETR_MOUSE	P91435 mus musculus
23	532.5	21.8	324	1	TEST_MOUSE	Q91hj7 mus musculus
24	527	21.6	761	1	PLMN_HORSE	P0801 equus caballus
25	526	21.5	338	1	PLMN_PIG	P08667 sus scrofa
26	523.5	21.4	790	1	ST14_HUMAN	P0801 equus caballus
27	523	21.4	855	1	ST14_MOUSE	Q915y6 mus musculus
28	522.5	21.4	422	1	DESI1_HUMAN	Q91152 homo sapien
29	520.5	21.3	1042	1	CORI1_HUMAN	Q91955 homo sapien
30	511.5	20.9	314	1	TRYG_MOUSE	Q91q17 mus musculus
31	507	20.8	314	1	TEST_HUMAN	Q916m0 homo sapien
32	506.5	20.7	1113	1	CORI1_MOUSE	Q92119 mus musculus
33	505	20.7	875	1	NETR_HUMAN	Q95730 homo sapien

ALIGNMENTS

34	504	20.6	273	1	MCF7_MOUSE	MUS musculus
35	504	20.6	625	1	FA11_HUMAN	Homo sapiens
36	502	20.5	275	1	TRYT_CARPA	Canis familiaris
37	502	20.5	810	1	PLMN_HUMAN	Homo sapiens
38	500	20.5	810	1	PLMN_MOUSE	Mus musculus
39	499	20.4	343	1	PLMN_SHEEP	Ovis aries
40	499	20.4	273	1	TRYT_SHEEP	Ovis aries
41	499	20.4	810	1	PLMN_ERIEU	Oreamnos americanus
42	495.5	20.3	437	1	ACRO_RAT	Rattus norvegicus
43	495	20.3	270	1	TRYT_MERIN	Meriones unguiculatus
44	495	20.3	810	1	PLMN_MACMU	Macaca mulatta
45	495	20.3	812	1	PLMN_BOVIN	Bos taurus

RESULT 1

TMS3_HUMAN

ID TMS3_HUMAN

AC P5727;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DB Transmembrane protease, serine 3 (EC 3.4.21.-) (Serine protease TADG-12) (Tumor associated differentially-expressed gene-12 protein).

GN TMFRS3 OR TAG12 OR ECHOS1.

OS Homo sapiens (Human).

OC Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1] NCBITaxID=9606;

RP SEQUENCE FROM N.A. (ISOFORMS A AND T).

RC TISSUE=Ovarian carcinoma;

RX MEDLINE=0521358; PubMed=11068177;

RA Underwood L.J., Shigemasa K., Tanimoto H., Beard J.B., Schneider E.N., Wang Y., Parmley T.R., O'Brien T.J., "Ovarian tumor cells express a novel multi-domain cell surface serine protease.", Biochim. Biophys. Acta 1502:337-350(2000).

RT [2]

RN RY SEQUENCE FROM N.A. (ISOFORMS A AND D), AND VARIANT ILE-53.

RX MEDLINE=20578149; PubMed=11137999;

RA Scott H.S., Kadon J., Wattenthaler M., Shibuya K., Berry A., Chraast R., Giupponi S., Radhakrishna U., Minoshima S., Akasaki S., Marzella P.L., Kudoh J., Younis F., Nahdi S.Q., Radhakrishna U., Papasavvas M.P., Gehrig C., Rossier C., Korostishhevsky M., Gal A., Shimizu N., Bonne-Tamir B., Antonaratis S.E., "Insertion of beta-satellite repeats identifies a transmembrane protease causing both congenital and childhood onset autosomal recessive deafness.", Nat. Genet. 27:59-63 (2001).

RT RT

RN "The transmembrane serine protease (TMFRS3) mutated in deafness DNFBB10 activates the epithelial sodium channel (ENaC) in vitro.", Hum. Mol. Genet. 11:2849-2856 (2002).

RP [3]

RN SUBCELLULAR LOCATION, AND FUNCTION IN ENaC CLEAVAGE.

RX MEDLINE=22281255; PubMed=12393794;

RA Giupponi M., Vuagniaux G., Wattenthaler M., Vazquez M.,

RA Dougherty L., Scamuffa N., Guida E., Okui M., Rossi C., Hancock M., Buceta K., Reynaud A., Hammel B., Marzella P.L., Kudoh J., Shimizu N., Scott H.S., Antonaratis S.E., Rossier B.C.; "The transmembrane serine protease (TMFRS3) mutated in deafness DNFBB10 activates the epithelial sodium channel (ENaC) in vitro.", Hum. Mol. Genet. 11:2849-2856 (2002).

RP [4]

RN VARIANTS DFBNB/DFNB10 CYS-251 AND LEU-404.

RA Masoudi S., Antonaratis S.E., Schwede T., Ghorbali A.M., Gratrix M.,

RA Rossier C., Scott H.S., Drira M., Elgated A., Wattenthaler M.,

RA "Novel missense mutations of TMFRS3 in two consanguineous Tunisian families with non-syndromic autosomal recessive deafness.", Hum. Mutat. 18:101-108 (2001).

RP [5]

RN VARIANTS DFBN8/DFBN10 TRP-109, PHE-194 AND ARG-407, AND VARIANTS

RP

Query Match Similarity 99.6%; Score 2432.5; DB 1; Length 454;
 Best Local Similarity 99.8%; Pred. No. 2.7e-198; Indels 1; Gaps 1;
 Matches 453; Conservative 0; Mismatches 0;

Qy 1 MGENDPPAVAPEPESRSLFGLDDIKTISPVAPDAAVAQQLSLPLKPFPIITVIGIAlI 60
 Db - 1 MGENDPPAVAPEPESRSLFGLDDIKTISPVAPDAAVAQQLSLPLKPFPIITVIGIAlI 60
 DR 61 LALAIGGIHFDGSKYRCSSEFKCTELIARDGYSCKDGEDEYRCVRGGONAVLOF 120
 DR 61 LALAIGGIHFDGSKYRCSSEFKCTELIARDGYSCKDGEDEYRCVRGGONAVLOF 120
 DR 61 TAASWKTMCSDWKGHYANVACAQGLFPSTVSSDNLRVSSLEGQFREEFVPSIDHLPLDK 180
 DR 61 TAASWKTMCSDWKGHYANVACAQGLFPSTVSSDNLRVSSLEGQFREEFVPSIDHLPLDK 180
 DR 181 VIALHSVYREGCASHVTLQTAGCHRGYSSRIUGGAMSLLSQWPQAISLQPOGYH 240
 DR 181 VIALHSVYREGCASHVTLQTAGCHRGYSSRIUGGAMSLLSQWPQAISLQPOGYH 240
 DR 241 LGGSVITPLWIIATAAHCVYDILPKSWTIQVGLSLLDPAHSLVEKTVVHSKYKPR 300
 DR 241 LGGSVITPLWIIATAAHCVYDILPKSWTIQVGLSLLDPAHSLVEKTVVHSKYKPR 300
 DR 301 LGNDIAMKLAGPLTFNEMIQVCLPNSENFPDGKVCMWSGATEDGAGDASVLTNA 359
 DR 301 LGNDIAMKLAGPLTFNEMIQVCLPNSENFPDGKVCMWSGATEDGAGDASVLTNA 359
 DR 360 AVPLISNKICHRDVYCGSIISPSMLCAGYLTCGVDSQGDSGGPLYCQERRLWKLUGATS 419
 DR 361 AVPLISNKICHRDVYCGSIISPSMLCAGYLTCGVDSQGDSGGPLYCQERRLWKLUGATS 420
 DR 420 FGIGCAEVNPKPGVYTRUTSFIDWHEQMERDIFT 453
 DR 421 FGIGCAEVNPKPGVYTRUTSFIDWHEQMERDIFT 454

RESULT 2

TMS3_MOUSE	Q8VDB0;	STANDARD;	PRT;	453 AA.
ID	OBK1TO;			
AC				
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2004 (Rel. 42, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Transmembrane protease, serine 3 (EC 3.4.21.-).			
GN	TMRSS3			
OS	Mus musculus (Mouse)			
OC	Mammalia; Eutheria; Rodentia; Sciurognathli; Muridae; Murinae; Mus.			
OX	NCBI_TaxID:10090;			
RN	[1]			
RP	SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND FUNCTION IN ENAC			
CL	CLEavage			
DR	PMID:12281255; PubMed=12393794;			
RX	Guipponi M., Vuagniaux G., Wattenthaler M., Shibusawa K., Vazquez M., Dougherty L., Scamuffa N., Guida B., Okui M., Rossier C., Hancock M., Buchet K., Raymond A., Hummer E., Marcelli L., Rudoh J., Shimizu N., Scott H.S., Antonarakis S.E., Rossier B.C.; "The transmembrane serine protease (TMRSS3) mutated in deafness." DFNB8/10 activates the epithelial sodium channel (ENaC) in vitro."; Hum. Mol. Genet. 11:2839-2846 (2002).			
CC	-!- FUNCTION: Probable protease. Seems to be capable of activating ENaC.			
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic reticulum.			
CC	-!- TISSUE SPECIFICITY: Expressed in the spiral ganglion, the cells supporting the organ of Corti and the stria vascularis.			
CC	-!- PTM: Undergoes autoproteolytic activation.			
CC	-!- SIMILARITY: Belongs to Peptidase family SI.			
CC	-!- SIMILARITY: Contains 1 LDL-receptor class A domain.			
CC	-!- SIMILARITY: Contains 1 SCR domain.			

Query Match Similarity 91.1%; Score 2226; DB 1; Length 453;
 Best Local Similarity 89.2%; Pred. No. 8.1e-181; Indels 0; Gaps 0;
 Matches 404; Conservative 24; Mismatches 25; Delins 0;

Qy 1 MGENDPPAVAPEPESRSLFGLDDIKTISPVAPDAAQQLSLPLKPFPIITVIGIAlI 60
 Db 1 MGENDPPAEEAPFSRSLFGLDDIKTISPVAPDAAQQLSLPLKPFPIITVIGIAlI 60
 DR 61 LALAIGGIHFDGSKYRCSSEFKCTELIARDGYSCKDGEDEYRCVRGGONAVLOF 120
 DR 61 LALAIGGIHFDGSKYRCSSEFKCTELIARDGYSCKDGEDEYRCVRGSQDAAQLQVF 120
 DR 121 TAASWKTMCSDWKGHYANVACAQGLFPSTVSSDNLRVSSLEGQFREEFVSTHLLPDK 180
 DR 121 TAASWKTMCSDWKGHYANVACAQGLFPSTVSSDNLRVSSLEGQFREEFVSTHLLPDK 180

Y	181	VTAIHLHSVYVREGCAGSHVYTLOCTACGHRRGYSRIVCGNMSSLISQFWOASIQFOGYH Y	240
b	181	VTAIHLHSVYVREGCAGSHVYTLOCTACGHRRGYSRIVCGNMSSLISQFWOASIQFOGYH Y	240
Y	241	LGGGSVITPLWIIIAHCVYDLYBKSWTIQLQVYWLSDNPAWSHLVEKIVHSSKYKPKR Y	300
b	241	LGGGSVITPLWIIIAHCVYDLYBKSWTIQLQVYWLSDNPAWSHLVEKIVHSSKYKPKR Y	300
Y	301	LGNDIALMKLAKGPFNEMIOPVCPDNSEENFPDKRVCWTSGWATEDEGDASPVLNAA Y	360
b	301	LGNDIALMKLAKGPFNEMIOPVCPDNSEENFPDKRVCWTSGWATEDEGDASPVLNAA Y	360
Y	361	VPLISNKICNHRDVYGGIISPSPMLCAGYLTCGGVDSCQGDGGPLVQCCRRLWKLVGATSF Y	420
b	361	VPLISNKICNHRDVYGGIISPSPMLCAGYLTCGGVDSCQGDGGPLVQCCRRLWKLVGATSF Y	420
Y	421	GIGCAEVNKQGVYTVTTSFIDWHEQMERDIKT Y	453
b	421	GIGCAEVNKQGVYTVTTSFIDWHEQMERDIKT Y	453

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CC	EMBL; U75329; AAC51784.1; -.	DR	
CC	EMBL; AF123453; AAD37117.1; -.	DR	
CC	EMBL; AF210487; AAC29280.1; -.	DR	
CC	HSSP; P00763; 1DPO.	DR	
CC	MEROPS; SOL_247; -.	DR	
CC	GENE; HGNC:11876; TMRSS2.	DR	
CC	MIM: 602050; -.	DR	
CC	GO; GO:0005987; C:integral to plasma membrane; TAS.	DR	
CC	GO; GO:0008236; F:Barine-type peptidase activity; TAS.	DR	
CC	InterPro; IPR09003; Cys_Ser_trypsin.	DR	
CC	InterPro; IPR02172; LDL_receptor_A.	DR	
CC	InterPro; IPR01254; Peptidase_S1.	DR	
CC	InterPro; IPR01314; Peptidase_S1.	DR	
CC	InterPro; IPR01190; Ssrc_receptor.	DR	
CC	pfam; PF00089; trypsin_1.	DR	
CC	PRINTS; PROT722; CHNOTRIPSIN.	DR	
CC	SMART; SM00192; LDDA; 1.	DR	
CC	SMART; SM00202; SR; 1.	DR	
CC	SMART; SM00020; TRYPSIN_SP_C; 1.	DR	
CC	PROSITE; PS011209; LDDRA; 1; 1.	DR	
CC	PROSITE; PS50068; LDDRA; 2; 1.	DR	
CC	PROSITE; PS000420; SRCR_1; FALSE_NEG.	DR	
CC	PROSITE; PS50287; SRCR_2; 1.	DR	
CC	PROSITE; PS50240; TRYPSIN_DOM; 1.	DR	
CC	PROSITE; PS00134; TRYPSIN_HIS; 1.	DR	
CC	PROSITE; PS00135; TRYPSIN_SER; 1.	DR	
KW	Hydrolase; Serine_protease; Transmembrane; Signal-anchor; Zymogen;		
KW	Polymorphism; 1	255	TRANSMEMBRANE PROTEASE, SERINE 2, NON-CATALYTIC CHAIN
FT	CHAIN	256	TRANSMEMBRANE PROTEASE, SERINE 2,
FT	PT DOMAIN	1	CATALYTIC CHAIN
FT	PT TRANSMEM	85	CYTOPLASMIC (POTENTIAL)
FT	PT DOMAIN	106	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT	PT DOMAIN	112	(POTENTIAL).
FT	PT DOMAIN	112	EXTRACELLULAR (POTENTIAL).
FT	PT DOMAIN	149	LDL-RECEPTOR CLASS A.
FT	PT DOMAIN	150	SRCR.
FT	PT DOMAIN	242	SERINE PROTEASE
FT	ACT SITE	296	CHARGE RELAY SYSTEM (BY SIMILARITY)
FT	ACT SITE	345	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT	ACT SITE	441	(POTENTIAL).
FT	ACT SITE	255	CHARGE RELAY SYSTEM.
FT	DISULFID	113	CLEAVAGE (POTENTIAL).
FT	DISULFID	120	SRCR.
FT	DISULFID	133	CHARGE RELAY SYSTEM.
FT	DISULFID	148	CHARGE RELAY SYSTEM.
FT	DISULFID	172	CHARGE RELAY SYSTEM.
FT	DISULFID	185	CHARGE RELAY SYSTEM.
FT	DISULFID	244	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	281	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	410	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	437	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	465	INTERCHAIN (BY SIMILARITY).
FT	CARBONYD	213	N-LINKED (GLCNAC, . .) (POTENTIAL).
FT	CARBONYD	249	N-LINKED (GLCNAC, . .) (POTENTIAL).
FT	VARIANT	449	N->N (IN dBSNP:10566602).
FT	MUTAGEN	255	/PTID:YAR011692
FT	MUTAGEN	441	R->Q: LOSS OF CLEavage.
FT	CONFLICT	160	S->A: LOSS OF ACTIVITY.
FT	CONFLICT	242	M->V (IN REF. 3).
FT	CONFLICT	329	I->L (IN REF. 1).
FT	CONFLICT	489	E->Q (IN REF. 1).
FT	CONFLICT	491	RAD->KAN (IN REF. 1).
SQ	SEQUENCE	492 AA;	CAB44PD173A9076B CRC64;
SQ	SEQUENCE	53891 MW;	
Query Match		36.1%	Score 892; DB 1; Length 492;
Best Local Similarity		45.7%	Prd. No. 5 2e-67;
Best Local Similarity		45.7%	Microtub
Best Local Similarity		45.7%	Indels 20. Gaps

between the Swiss Institute of Bioinformatics and the EMBL Outstation -

Sequence Comparison Results							
Query Sequence		Target Sequence		Comparison Details			
	Sequence		Sequence	Score	Length	Mismatches	Gaps
FT	DISURFID	76	125	BY SIMILARITY.			
FT	DISURFID	119	138	BY SIMILARITY.			
FT	DISURFID	132	147	BY SIMILARITY.			
FT	DISURFID	171	230	BY SIMILARITY.			
FT	DISURFID	184	240	BY SIMILARITY.			
FT	DISURFID	243	363	INTERMIXED (BY SIMILARITY).			
FT	DISURFID	279	295	BY SIMILARITY.			
FT	DISURFID	408	424	BY SIMILARITY.			
FT	DISURFID	435	463	BY SIMILARITY.			
FT	CARBHYD	111	111	N-LINKED (GLCNAC, . . .) (POTENTIAL).			
FT	CARBHYD	212	212	N-LINKED (GLCNAC, . . .) (POTENTIAL).			
FT	CARBHYD	474	474	N-LINKED (GLCNAC, . . .) (POTENTIAL).			
FT	CONFFLICT	122	122	S -> L (IN REF. 3).			
FT	CONFFLICT	178	178	S -> N (IN REF. 3).			
FT	CONFFLICT	320	320	Y -> H (IN REF. 1).			
FT	CONFFLICT	474	474	N -> D (IN REF. 1).			
SQ	SEQUENCE	490 AA:	53479 MW:	07DB03EA4D8A1A9 CRC64;			
Query Match							
Best Local Similarity		Score		Pred. No. 2e-66; Indels 66; Gaps 13;			
Matches 193; Conservative		66; Mismatches 146;					
Qy	28	PVAPADAVAAQILSSLPLKFFPIIV-----IGI-----A 58					
Db	31	PVAPNG-----YNYLPAQYYPSPPPQYAPRITQDASTSVTHTHKSSGAPCTSKSKKS 83					
Qy	59	LTLALAGLGI-----HEDCS-SKYRGRSFSFKCIELTARCDDGSDCDKGED 103					
Db	84	LCLALALGTVLGAVALWRFWDSNCSESGRAACKDMGKNNFYSSQGPDQS 203					
Qy	104	EYRCYRVGQNQAVLQVFTA--ASWKTMCSDDWKHTYANVACQOLGP--SYSSDNTRVSS 160					
Db	144	ENFCVRFLQGSFLQVTSQRQKAWPYCQDDYSESGRAACKDMGKNNFYSSQGPDQS 203					
Qy	161	LEQPREEFVSDIDLPPDKVTAHLHSVYREGCAHGHHVTLQCTAGHRR-GYSRSRVG 219					
Db	204	GATSMFKLNIVSSRN--DLYKCDYHS---DSCSSMNKVSLRCIEGVRSLRVRQRRVG 256					
Qy	220	GANSLSOMPWQSLQFGYHLLGGSVTIPMLWIAAHCVYD-LYLPKSWTIQGVLY-S 276					
Db	257	GLNAPSGDWPKWQSLHVQVHVGVSGLITPENWVTAAHCVEPGLSGRYWTAFAGLIRQS 316					
Qy	277	LLDNPAPSLVHEVYHSHYKVKPRLGNDJALMKLAGPTTFNEMIQCYCLPNSSEBNPDGK 336					
Db	317	LMFY-GSHHQVERVSHYNDSTSNTKNDIALMKLOPLAFENDLVKPVCLPNPGMMUDLQ 375					
Qy	337	VCTISGWGATEDGDDASPYLNHAPLISNKIGNHRDVYGGTISPSMILCAGTLYGGYDSC 396					
Db	376	ECWISGWGATYEGRTSDLNAMVPLIEPSKNSRKYIYNLITAPICAGFLQGSYDSC 435					
Qy	397	QGDGGPLCYCQBERLWKLVGATSGFGIGCAEVNPKGYTYTRTSFLDWTHEQM 447					
Db	436	QGDGGPLCYTFLKGNIWWLJGDTSWGSGCAKLRPGVYGNVTFTDWIYQQM 486					
RESULT 5							
TMSS5	MOUSE						
ID	TMS5_MOUSE	STANDARD;	PRT;	455 AA.			
Q9E04	Q9E04 ; Q9ER02 ; Q9ER03 ;						
DT	16-OCT-2001 (Rel. 40, Created)						
DT	16-OCT-2001 (Rel. 40, Last sequence update)						
DT	28-FEB-2003 (Rel. 41, Last annotation update)						
DE	Transmembrane protease, serine 5 (EC 3.4.21.-) (spinesin).						
GN	TMPPSS5.						
OS	Mus musculus (Mouse).						
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;						
OX	NCBI_TaxID=10990;						
RN	[1]						
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).						
RC	TISSUE=Brain;						
RA	Mitui S., Yamaguchi N.;						
RT	"CDNA cloning of mouse spinein."						

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CC	EMBL;	AB28140;	BAB20375; 1;	-;
CC	HSSP;	P00763;	DPO,	
CC	DR	Gensw;	HGNC:14908;	TMPRSS5.
CC	DR	MIM;	606751;	-;
CC	DR	MEROPS;	S01.313;	-;
CC	DR	InterPro;	IPR00903;	Cys Ser trypsin.
CC	DR	InterPro;	IPR001254;	Peptidase_S1.
CC	DR	InterPro;	IPR001314;	Peptidase_S1A.
CC	DR	InterPro;	IPR001190;	Sercr_receptor.
CC	DR	Pfam;	PF00089;	trypsin_1.
CC	DR	DR	SMART;	SM00020; TRYD_SPC_1.
CC	DR	DR	PROSITE;	PS500240; TRYPSIN_DOM; 1.
CC	DR	DR	PROSITE;	PS000144; TRYPSIN_HIS; 1.
CC	DR	DR	PROSITE;	PS000135; TRYPSIN_SER; 1.
CC	DR	DR	PROSITE;	PS000420; SRCR_1; FALSE_NEG.
CC	DR	DR	PROSITE;	PS50287; SRCR_2; FALSE_NEG.
CC	KW	Hydrolase; Serine Protease; Transmembrane; Signal-anchor;		
CC	KW	Glycoprotein.		
FT	DOMAIN	1	49	CYTOSPLASMIC (POTENTIAL).
FT	TRANSMEM	50	70	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT	FT	71	457	(POTENTIAL).
FT	FT	112	207	EXTRACELLULAR (POTENTIAL).
FT	FT	218	457	SRCR.
FT	ACT_SITE	258	258	SERINE PROTEASE.
FT	ACT_SITE	308	308	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	405	405	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	217	218	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	DISULFID	135	196	CLEAVAGE (POTENTIAL).
FT	DISULFID	148	206	BY SIMILARITY.
FT	DISULFID	209	328	BY SIMILARITY.
FT	DISULFID	243	259	BY SIMILARITY.
FT	DISULFID	374	390	BY SIMILARITY.
FT	DISULFID	401	429	BY SIMILARITY.
FT	CARBODY	163	163	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBODY	170	170	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBODY	195	195	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBODY	319	319	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBODY	375	375	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	457 AA;	49574 MW;	6440648498542651 CRCE4;
Query Match				Score 689.5 ; DB 1; Length 457;
Best Local Similarity				
Matches 149;	Conservative	35.2%;	Pre. No. 9.4e-51;	
Qy	Db	51	VIGALGLIAGAGGSWLLV---	LYLCPAASQPI-----GTQDEBETISCESEA SA 98
Qy	Db	99	EEBALPALKTVYSRINSEDFLLEAQYRDQPRMLVCHEGWSPALGLQTCWSLGHRLTH 158	
Qy	Db	113	QNAVL-----QVTAASPKTMKCDSGKRYCRSSFKCTELIARDGVSDCRQGEDEYRCVRVG 112	
Qy	Db	153	SDMLRVSSLEGPREEFYFSDHLLPDKKVTAALHSVSYREGCAGSHVNTLQCTAGHRRG 212	
Qy	Db	159	HKGVNLTDIKLNSSQEAQLSPRIGG---FLEAWQPNNTCSQQVSLRCSECG-ARP 213	
Qy	Db	213	YSSRTIVGNNMLSLSQWPWQASLQFGYHLGGSVITPLMIIATAHVCVYDLYLPK-SWTI 270	
Qy	Db	214	LASRTIVGGSVAPGVQASVALFRITCGGSVLAAPRNVTAAHCMSFLRARISSWRV 273	
Qy	Db	271	QVGLSV-LIDNPAPSHLVEKIVTHSKYKEPKRLGNDIAMLKLGPITFNEMIQPVCLPNE 329	
Qy	Db	274	HAGLVSHSAVRPHQGALVERIIPHPLYSQNHDYVALLPLQTANLNFSDTVGAVCLPAKE 333	

330	DY	ENFPDGKVCWTSGMATEDGGD-ASPVLNHAAPLISNKINHRDYGGIISPMLCAGY	388
334	Db	QHPKGSPCWCSSWGHHTPSHTYSIDMLOQDTVPLFSTOLCNSSCTYSGATPMLCAGY	393
389	DY	LTTGGVDSCQGDSGGLYCOERRLWKLGYATSGIGCAEVNPKGYTRVTSFELDWTHEOME	448
394	Db	LDGRADACQGDGGPLVCPDGDITWRLVGVSVSRAEAPNHPGVYAKVAEFLDWHDQA	453
449	DY	RDL 451	
454	Db	DSL 456	
RESULT 7			
MOUSE	4C	QBVCA5;	SEQUENCE FROM N.A.
MOUSE	4C	STANDARD;	SEQUENCE FROM N.A.
		PRT;	TISSUE=breast tumor;
		435 AA.	MEDLINE=223120257; PubMed=12477932;
			STRaussberg R.I., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
			Klauschner S.F., Collings F.S., Wagner L., Spener C.M., Schaefer C.F., Bhat N.K.,
			Alekschul S.F., Zeeberg B., Buetow K.H., Max S.I., Wang J., Hsieh P.,
			Hopkins R.F., Jordan H., Moore T., Rubin G.M., Hong L.,
			Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E.,
			Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
			Brownstein M.J., Jsdin T.B., Toshiyuki S., Carninci P., Mullaly S.J.,
			Raha S., Locqueur N.A., Peters R.D., Abramson R.D., McEwan P.J.,
			Boesk S.A., McEwan P.J., McErlean K.J., Malek J.A., Gunnarsson P.H.,
			Richards S., Worley K.C., Hale S., Garcia F.M., Gay L.J., Hulyk S.W.,
			Villalon D.K., Munro D.M., Sodergreen B.J., Lu X., Gibbs R.A.,
			Faley J., Heaton E., Kerteszen M., Madan A., Rodriguez S., Sanchez A.,
			Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
			Balesky R.W., Touchman J.W., Grimes B.D., Dickson M.C.,
			Rodriguez A.C., Grimwood J., Schnitz J., Myers R.M., Butterfield Y.S.N., Krzwicki M.I., Skalska U., Smilis D.E.,
			Schernich A., Schein J.B., Jones S.J.M., Marras M.A.,
			ScHERRT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"
			Proc. Natl. Acad. Sci. U.S.A. 99: 16899-16903 (2002)
			-!- FUNCTION: Probable protease. Seems to be capable of activating ENaC.
	CC	-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).	
	CC	-!- SIMILARITY: Belongs to peptidase family S1.	
	CC	-!- SIMILARITY: Contains 1 LDL-receptor class A domain.	
	CC	-!- SIMILARITY: Contains 1 SRCR domain.	
	CC		
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	CC		

RESULT 9
 ID_ENTK_BOVIN STANDARD; PRT; 1035 AA.
 AC_P98072; Rel. 33, Created)
 DT_01-FEB-1996 (Rel. 33, Last sequence update)
 DT_01-FEB-1996 (Rel. 43, Last annotation update)
 DE_Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase).
 PRSS7 OR ENTK.
 GN_Os taurinus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bos taurus; Bos. NCBI_TaxID=9913;
 RN_1
 RP_SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC_TISSUE=budenium;
 MEDLINE94329561; PubMed=8052624;
 RA_Kitamoto Y., Yuan X., Wu Q., McCourt D.W., Sadler J.E.; "Enterokinase, the initiator of intestinal digestion, is a mosaic protease composed of a distinct assortment of domains.", Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
 RL_RN_801-1135 AND PARTIAL SEQUENCE.
 RX_MEDLINE94043122; PubMed=80226855;
 RA_Lavallie E.R., Rehemtulla A., Racie L.A., DiBlasio E.A., Ferenz C., Grant K.L., Light A., McCoy J.M.; "Cloning and functional expression of a cDNA encoding the catalytic subunit of bovine enterokinase.", J. Biol. Chem. 268:23311-23317(1993).
 RN_3
 RP_SEQUENCE OF 801-827.
 RC_ISSUE=Intestine; MEDLINE9218915; PubMed=1799406;
 RA_Light A., Janska H.; "The amino-terminal sequence of the catalytic subunit of bovine enterokinase.", J. Protein Chem. 10:475-480(1991).
 RL_Proteolytic proenzymes for initiating activation of pancreatic trypsinogen. It catalyzes the conversion of trypsinogen to trypsin which in turn activates other proenzymes including chymotrypsinogen, procarboxypeptidases, and proelastases.
 CC_ALTERNATIVE ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in trypsinogen.

CC_- SUBUNIT: Heterodimer of a catalytic (light) chain and a multi-domain (heavy) chain linked by a disulfide bond.
 CC_- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC_- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Name=long;
 IsoID=P88072-1; Sequence=Displayed;

CC_Name-Short:
 CC_1b0d=p88072-2; Sequence=vsp_003386;
 CC_- TISSUE SPECIFICITY: Intestinal-brush border.
 CC_- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS CLEAVED BY A TRYPSIN-LIKE PROTEASE.
 CC_- SIMILARITY: Belongs to peptidase family S1.
 CC_- SIMILARITY: Contains 2 CUB domains.

CC_- SIMILARITY: Contains 2 LDL-receptor class A domains.
 CC_- SIMILARITY: Contains 1 MAM domain.
 CC_- SIMILARITY: Contains 1 SEA domain.
 CC_- SIMILARITY: Contains 1 SRCR domain.
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 CC DR_EMBL; U09859; AAB00261;
 CC DR_EMBL; L19663; AAA16035.1;
 CC DR_PIR; A43090; A43090.
 CC DR_PDB; 1EKB; 14-Oct-99.
 CC DR_MEROPS; S01_156; -.
 CC DR_InterPro; IPR000859; CUB.
 CC DR_InterPro; IPR009003; CYS_Ser trypsin.
 CC DR_InterPro; IPR020212; LDL_receptor_A.
 CC DR_InterPro; IPR00988; MAM_domain.
 CC DR_InterPro; IPR001254; Peptidase_S1.
 CC DR_InterPro; IPR001314; Peptidase_S1A.
 CC DR_InterPro; IPR000862; SEA_domain.
 CC DR_InterPro; IPR001130; SRCR_receptor.
 CC DR_Pfam; PF00431; CUB_2.
 CC DR_Pfam; PF00057; Ig_recept_a_2.
 CC DR_Pfam; PF00629; MAM_1.
 CC DR_Pfam; PF01390; SEA_1.
 CC DR_Pfam; PF00530; SRCR_1.
 CC DR_Pfam; PF00089; trypsin_1.
 CC DR_PRINTS; PRO0722; CHYMOTRYPSIN.
 CC DR_PRINTS; PRO0261; LDLRECEPTOR.
 CC DR_SMART; SN00042; CUB_2.
 CC DR_SMART; SN00192; LDLia_2.
 CC DR_SMART; SN00117; MAM_1.
 CC DR_SMART; SN0200; SEA_1.
 CC DR_SMART; SN00202; TRYD_SPC_1.
 CC DR_SMART; SN001180; CUB_2.
 CC DR_PROSITE; PS01209; LDLRA_1; 2.
 CC DR_PROSITE; PS50068; LDLRA_2; 2.
 CC DR_PROSITE; PS00740; MAM_1; 1.
 CC DR_PROSITE; PS50060; MAM_2; 1.
 CC DR_PROSITE; PS50024; SEA_1.
 CC DR_PROSITE; PS50020; SRCR_1; FALSE_NEG.
 CC DR_PROSITE; PS50087; SRCR_2; 1.
 CC DR_PROSITE; PS50240; TRYPSIN_DOM; 1.
 CC DR_PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC DR_PROSITE; PS00135; TRYPSIN_SER; 1.
 CC KW_Signal-anchor; Glycoprotein; Myristate; Hydrolase; Serine protease; Zymogen; Transmembrane; Repeat; Alternative splicing; 3D_structure; Lipoprotein.

NON-CATALYTIC CHAIN (HEAVY CHAIN).
 FT_CHAIN 1 800
 FT_DOMAIN 801 1035
 FT_DOMAIN 1 18
 FT_TRANSMEM 19 47
 FT_DOMAIN 48 1035
 FT_DOMAIN 54 169
 FT_DOMAIN 197 238
 FT_DOMAIN 240 350
 FT_DOMAIN 258 520
 FT_DOMAIN 540 650
 FT_DOMAIN 657 695
 FT_DOMAIN 694 767
 FT_DOMAIN 801 1035
 FT_ACT_SITE 841 841
 FT_ACT_SITE 892 892
 FT_ACT_SITE 987 987
 FT_LIPID 2 2
 FT_DISUFID 199 212

SERINE PROTEASE.
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CUB_1.
 MAM.
 CUB_2.
 LDLRECEPTOR CLASS A_2.
 SERINE PROTEASE.
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CUB_1.
 MAM.
 CUB_2.
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 N-myristoyl_glycine (Potential).
 BY SIMILARITY.

FT	DISULFID	206	225	BY SIMILARITY.
FT	DISULFID	219	236	BY SIMILARITY.
FT	DISULFID	659	671	BY SIMILARITY.
FT	DISULFID	666	684	BY SIMILARITY.
FT	DISULFID	678	693	BY SIMILARITY.
FT	DISULFID	788	912	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	826	842	BY SIMILARITY.
FT	DISULFID	926	993	BY SIMILARITY.
FT	DISULFID	957	972	BY SIMILARITY.
FT	DISULFID	983	1011	BY SIMILARITY.
FT	CARBONYD	116	116	(POTENTIAL).
FT	CARBONYD	147	147	N-LINKED (GLCNAC. . .)
FT	CARBONYD	170	170	N-LINKED (GLCNAC. . .)
FT	CARBONYD	194	194	(POTENTIAL).
FT	CARBONYD	233	233	N-LINKED (GLCNAC. . .)
FT	CARBONYD	263	263	(POTENTIAL).
FT	CARBONYD	264	264	N-LINKED (GLCNAC. . .)
FT	CARBONYD	404	404	(POTENTIAL).
FT	CARBONYD	456	456	N-LINKED (GLCNAC. . .)
FT	CARBONYD	486	486	(POTENTIAL).
FT	CARBONYD	519	519	N-LINKED (GLCNAC. . .)
FT	CARBONYD	550	550	(POTENTIAL).
FT	CARBONYD	646	646	N-LINKED (GLCNAC. . .)
FT	CARBONYD	698	698	(POTENTIAL).
FT	CARBONYD	722	722	N-LINKED (GLCNAC. . .)
FT	CARBONYD	741	741	(POTENTIAL).
FT	CARBONYD	762	762	N-LINKED (GLCNAC. . .)
FT	CARBONYD	864	864	(POTENTIAL).
FT	CARBONYD	903	903	N-LINKED (GLCNAC. . .)
FT	CARBONYD	965	965	(POTENTIAL).
FT	VARSPLIC	166	192	Missing Lin Isoform Short).
FT	CONFFLICT	808	808	/FTid=VSP 005386.
FT	SEQUENCE2	1035	AA;	R -> Y (IN REF. 3),
SQ		114887	MW;	E207970B08296E13 CRC64;
Query	Match	27.4%	Score 669 5;	DB 1; Length 1035;
Best Local Similarity	37.0%	Pred. 1.2e-48;	DB 1;	Gaps 14;
Matches	146;	Conservative	70;	Mismatches 146;
DB	656	GGGTHEDC-SGKYKRCRSSPKCIELJARCDGVSDCKDGEDEYRCYRV-	--GGGNAVILQVF	120
DB	652	GLGIPPEPKEDNFQCKDGG-ECIPLVNLCDFPHCKDGGSDAEHCYVRLNGTDTDSCLVQFLQR	710	
Qy	121	TAASWKTMOSDDKGHYANVACAGLQPFPSVYSSDNLRVSSLEGQPREFNSIDHLLPDKK	180	
DB	711	IQS1WHVAQENNTQISDVSQCLGLGT-GNSSSVPTFSTGG--GPYVNNLSNPWPQAS	758	
Qy	181	VITALJHSVVY-REGCASHVVTQCT-ACGHR--RGYSSRTVGGMNSLLSOPWPQAS	233	
DB	759	-TAPNGSLLTPSOCLLEDLILQCNYSCKGLLVTVQSPKIVGGDSREGAMPWVVA	817	
Qy	234	LQFOGYHLCCGSVITPLWIIATAAHCVIDL-Y-PKSWTIYGL--VSLLDNP-APSHLVEK	289	
DB	818	LYFDDQQVCGASLVSRDWVSAH-VYGRANNEPSKWKAVGLRASNLTSPQIETRLDQ	877	
Qy	290	IYTHSKYKPKRLGNDIANLMKLQPLTENEMIQPVCLPNSENFKPGKVKCWTSGNCATEDG	349	
DB	878	IVNPHNFRKRKNDIANMHNLMKVNTDYLQPIQUEENQVFPFGRCISGAGLTYQ	937	
Qy	350	GDASPVLNHAAPLISNKICNHR-DVYGGIISPMSLCAGLTGVDGSDGGBLVQCE	408	
DB	938	GSTDVLDLQADVPPLSNKQCCQOQMPBEYN--ITENNVCAVYEGGGVDSLQSDSGGMLMCQE	995	
Qy	409	RRLMKLVGATSPFGCAENPKGTYTRVTSFLDWI	443	
DB	986	NNRRLLAGVTSSEYQOCALPRPGYAYARPPETEWI	1030	

```

RESULT 10
ENTK_HUMAN STANDARD; PRT; 1019 AA.
ID ENTK_HUMAN P98073 AC DT 01-FEB-1996 (Rel. 33. Created)
CC -|- SIMILARITY: Contains 2 LDL-receptor class A domains.
CC -|- SIMILARITY: Contains 1 MAM domain.
CC -|- SIMILARITY: Contains 1 SEA domain.
CC -|- SIMILARITY: Contains 1 SRCR domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the European Bioinformatics Institute (EMBL-EBI) and the
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PT	CHAIN	1	784	NON-CATALYTIC CHAIN (HEAVY CHAIN).
FT	CHAIN	785	1013	CATALYTIC CHAIN (LIGHT CHAIN).
PT	DOMAIN	1	18	CITOPLASMIC (POTENTIAL).
FT	TRANSMEM	19	47	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
PT	DOMAIN	48	1019	(POTENTIAL).
PT	DOMAIN	52	156	EXTRACELLULAR (POTENTIAL).
PT	DOMAIN	53	156	SPA

NON-CATALYTIC CHAIN (HEAVY CHAIN).
CATALYTIC CHAIN (LIGHT CHAIN).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SERPENTINE.

```

EMBL; U09860; AAC50138.1; -.
EMBL; Y19124; CAB65555.1; -.
EMBL; Y19125; CAB65555.1; JOINED.
EMBL; Y19126; CAB65555.1; JOINED.
EMBL; Y19127; CAB65555.1; JOINED.
EMBL; Y19128; CAB65555.1; JOINED.
EMBL; Y19129; CAB65555.1; JOINED.
EMBL; Y19130; CAB65555.1; JOINED.
EMBL; Y19131; CAB65555.1; JOINED.
EMBL; Y19132; CAB65555.1; JOINED.
EMBL; Y19133; CAB65555.1; JOINED.
EMBL; Y19134; CAB65555.1; JOINED.
EMBL; Y19135; CAB65555.1; JOINED.
EMBL; Y19136; CAB65555.1; JOINED.
EMBL; Y19137; CAB65555.1; JOINED.
EMBL; Y19138; CAB65555.1; JOINED.
EMBL; Y19139; CAB65555.1; JOINED.
EMBL; Y19140; CAB65555.1; JOINED.
EMBL; Y19141; CAB65555.1; JOINED.
EMBL; Y19142; CAB65555.1; JOINED.
EMBL; Y19143; CAB65555.1; JOINED.
EMBL; AL163218; CAB90332.1; -.
EMBL; AL163217; CAB90339.1; -.
PTB; A56318; A56318.
HSRP; P00763; 1DPO.
MEROPS; S01_156; -.
GeneW; HGNC:9490; PRSS7.
NLM; 606635; -.
MIM; 222200; -.
GO; GO:0005903; C-brush border; TAS.
InterPro; IPR00859; CDB.
InterPro; IPR00903; Cys_Ser_trypsin.
InterPro; IPR00212; LDL_receptor_A.
InterPro; IPR00998; NAM_domain.
InterPro; IPR00125; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR000082; SEP_domain.
InterPro; IPR001190; Srr_receptor.
Pfam; PF00431; CUB_2.
Pfam; PF00057; ldl_recept_a_2.

```

FT	CHAIN	1	784
FT	CHAIN	785	1019
FT	DOMAIN	1	18
FT	TRANSMEM	19	47
FT	DOMAIN	48	1019
FT	DOMAIN	53	1019
FT	TRANSMEM	54	1019

F1	DOMAIN	182	223
FT	DOMAIN	225	334
FT	DOMAIN	342	504
FT	DOMAIN	524	634
FT	DOMAIN	641	679
FT	DOMAIN	678	771
FT	DOMAIN	785	1019
FT	ACT-SITE	825	825
FT	ACT-SITE	876	875
FT	ACT-SITE	971	971
FT	LIPID	2	2
FT	DISULFID	184	197
FT	DISULFID	191	210
FT	DISULFID	204	221
FT	DISULFID	643	655
FT	DISULFID	650	668
FT	DISULFID	662	677
FT	DISULFID	772	896
FT	DISULFID	810	826
FT	DISULFID	910	977
FT	DISULFID	941	956
FT	DISULFID	967	995
FT	CARBONYD	116	116
FT	CARBONYD	147	147
FT	CARBONYD	179	179
FT	CARBONYD	328	328
FT	CARBONYD	335	335
FT	CARBONYD	388	388
FT	CARBONYD	440	440
FT	CARBONYD	470	470
FT	CARBONYD	503	503
FT	CARBONYD	534	534
FT	CARBONYD	630	630
FT	CARBONYD	682	682
FT	CARBONYD	706	706
FT	CARBONYD	725	725
FT	CARBONYD	848	848
FT	CARBONYD	887	887
FT	CARBONYD	909	909
FT	CARBONYD	949	949
FT	CONFLICT	134	134
FT	CONFLICT	732	732
FT	CONFLICT	754	771

Query Match	27.
Best Local Similarity	37.
Matches 147; Conservative	
Y	67 LGIHFDC-SGKVRGR
b	67 : :
Y	637 LGIPPCPKADHFQCK
b	637 : :
Y	122 AASWETMCSDDWKGH
b	122 : :
Y	696 QSIWHTACENWTT
b	696 : :
Y	182 TALHSVYREGGAS
b	182 : :
Y	748 ---HULLTPQQCLC
b	748 : :
Y	237 QGYHUGGSVITPLW
b	237 : :
Y	805 GGRLLCGASLYSSD
b	805 : :
Y	293 HSKYKPKRGLNDIA
b	293 : :

RESULT 11

ENTK_PIG STANDARD; PRT; 1034 AA.

AC P98074; Created) DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase).

GN PRSS7 OR ENTK.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetariodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID:9823;

RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE-DOMAIN: mucosa;

RX MEDLINE=94327548; PubMed=8051081;

RA Matsushima M., Ichinose M., Yabagi N., Kakei N., Tsukada S., Niiki K., Kurokawa K., Tasiro K., Shiohawa K., Shinomoya K., Ueyama H., Inoue H., Takahashi T., Takahashi K., "Structural characterization of porcine enteropeptidase.";

RT J. Biol. Chem. 269(1994):19821-19821(1994).

RL Biochem. 269(1996):19821-19821(1996).

-!- FUNCTION: Responsible for initiating activation of pancreatic proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase A). It catalyzes the conversion of trypsinogen to trypsin which in turn activates other proenzymes including chymotrypsinogen, procarboxypeptidases, and proelastases.

-!- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in trypsinogen.

-!- SUBUNIT: Heterotrimer of a catalytic (heavy) chain, a multidomain (heavy) chain, and a mini chain.

-!- SUBCELLULAR LOCATION: Type II membrane protein (probable).

-!- PTM: The CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS CLEAVED BY A TRYPSIN-LIKE PROTEASE.

-!- PTM: THE MINI CHAIN MAY BE CLEAVED BY ELASTASE.

-!- SIMILARITY: Belongs to peptidase family S1.

-!- SIMILARITY: Contains 2 CUB domains.

-!- SIMILARITY: Contains 2 LDL-receptor class A domains.

-!- SIMILARITY: Contains 1 MAM domain.

-!- SIMILARITY: Contains 1 SEA domain.

-!- SIMILARITY: Contains 1 SRCR domain.

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CC EMBL: D30799; BA06459.1; - .

CC HSSP; P0763; IDPC.

CC MBROPS; S01_156; - .

CC InterPro; IPR000859; CUB.

CC InterPro; IPR009003; Cys_Ser_trypsin.

CC DR PRINTS; PRO0722; CHYMOTRYPSIN.

CC DR PRINTS; PRO0361; LDLRECEPTOR.

CC DR PRINTS; PRO0020; MAMDOMAIN.

CC DR SMART; SM00042; CUB; 2.

CC DR SMART; SM00192; LDIA; 2.

CC DR SMART; SM00137; MAM; 1.

CC DR SMART; SM00200; SEA; 1.

CC DR SMART; SM00202; SR; 1.

CC DR SMART; SM0020; TRYP_SPC; 1.

CC DR PROSITE; PS01180; CUB; 2.

CC DR PROSITE; PS01209; LDIA; 1; 2.

CC DR PROSITE; PS0068; LDIA; 2; 2.

CC DR PROSITE; PS00740; MAM; 1; 1.

CC DR PROSITE; PS0060; MAM; 2; 1.

CC DR PROSITE; PS50024; SEA; 1.

CC DR PROSITE; PS50287; SRCR; 2; FALSE_NEG

CC DR PROSITE; PS50240; TRYSIN_DOM; 1.

CC DR PROSITE; PS00134; TRYSIN_HIS; 1.

CC DR PROSITE; PS00135; TRYSIN_SER; 1.

CC KW Signal_anchor; Glycoprotein; Myristate; Hydrolase; Serine protease; Zymogen; Transmembrane; Repeat; Lipoprotein.

CC KW NON-CATALYTIC_M_CHAIN (MINI_CHAIN).

CC KW CATALYTIC_L_CHAIN (HEAVY_CHAIN).

CC KW CATALYTIC_L_CHAIN (LIGHT_CHAIN).

CC KW CYTOPLASMIC (POTENTIAL).

CC KW SIGNAL_ANCHOR (TYPE-II_MEMBRANE_PROTEIN) (POTENTIAL).

CC KW EXTRACELLULAR (POTENTIAL).

CC KW SPC.

CC CUB_1.

CC CUB_2.

CC LDL_RECECTOR_CLASS_A_1.

CC LDL_RECECTOR_CLASS_A_2.

CC SERINE_PROTEASE.

CC ACT_SITE 840 840

CC ACT_SITE 891 891

CC ACT_SITE 986 986

CC LIPID 199 2

CC DOMAIN 52 117

CC DOMAIN 118 799

CC DOMAIN 800 1034

CC DOMAIN 1 18

CC DOMAIN 19 47

CC DOMAIN 52 169

CC DOMAIN 197 238

CC DOMAIN 240 349

CC DOMAIN 357 519

CC DOMAIN 539 649

CC DOMAIN 656 694

CC DOMAIN 693 786

CC DOMAIN 800 1034

CC DOMAIN 219 236

CC DISULFID 658 670

CC DISULFID 665 683

CC DISULFID 677 692

CC DISULFID 199 212

CC DISULFID 206 225

CC DISULFID 219 225

CC DISULFID 658 670

CC DISULFID 665 683

CC DISULFID 677 692

CC DISULFID 787 911

CC DISULFID 825 841

CC DISULFID 925 992

CC DISULFID 958 971

CC DISULFID 1010 1010

CC CARBOHYD 116 116

CC CARBOHYD 147 147

CC CARBOHYD 170 170

CC CARBOHYD 194 194

CC CARBOHYD 283 283

CC CARBOHYD 343 343

CC CARBOHYD 350 350

CC CARBOHYD 403 403

CC CARBOHYD 455 455

CC CARBOHYD 485 485

CC CARBOHYD 518 518

CC CARBOHYD 549 549

CC CARBOHYD 645 645

CC CARBOHYD 697 697

CC CARBOHYD 701 701

PT CARBOHYD 721 721 N-LINKED (GLCNAC, .) (POTENTIAL).
 PT CARBOHYD 740 740 N-LINKED (GLCNAC, .) (POTENTIAL).
 PT CARBOHYD 761 761 N-LINKED (GLCNAC, .) (POTENTIAL).
 PT CARBOHYD 804 804 N-LINKED (GLCNAC, .) (POTENTIAL).
 PT CARBOHYD 863 863 N-LINKED (GLCNAC, .) (POTENTIAL).
 PT CARBOHYD 902 902 N-LINKED (GLCNAC, .) (POTENTIAL).
 PT CARBOHYD 964 964 N-LINKED (GLCNAC, .) (POTENTIAL).
 SQ SEQUENCE 1034 AA; 114776 MW; 0388C564CP64C368 CRC64;

Query Match_Similarity 27.2%; Score 663.5; DB 1; Length 1034;
 Best Local_Similarity 37.8%; Pred. No. 3.9e-48;
 Matches 149; Conservative 65; Mismatches 147; Indels 33; Gaps 14;

Qy 67 LGTHFDC-SGKYRCRSSFKCIBLARDGVSDCKDGEDEYRCVR---VGGQNAYLQVPT 121
 Qy 652 LGTPEPKEDDNFQENG-ECVLVLNLDGFSHICKDSDEAHCVRLNGTANNGLVQFRT 710
 Qy 122 AASWKTMCSSDDFKGHYANVACAQLGPFSYYSSDNLVYSSLEGQREFEVSIDHJLPDDKV 181
 Qy 711 QSIWHTAAENNTTQTSDDVCGOLIGLTGNSSMPF-FSSGGG---PFVFLN----- 757
 Db 758 TAAGSLLTATASQCFEDSLILQNCNRSGRKQVAQBSVPIKGENDSRREGAWPVVAL 817
 Qy 235 QFGQYALLGGSVITPLWITTAHCYDLYL-PKSWTIQVGL--VSLLDNP-APSHLVKEI 290
 Qy 818 YNGQLLQGASLNSRDLVSAAHCVYGRNLPSKWAILEHMTSNUTSPQIVTRLDEI 877
 Qy 182 TALHHSVTVY-RECCGASGHVTLQCT--ACGHR--RGYSSRIVGNNMSLISOMPQASL 234
 Qy 291 VHSKRYKRPLRNQDIAMLRKAGPLTFNEMIQPVCLPNSEANPPDGKVVCWTSWGATEDGG 350
 Db 878 VINPHYNRRKDSDIAMMHLLEFKVNYTDIOPCLPENQVPPGRICSTAGWGVKIYQG 937
 Qy 351 DASVPLNHAAPVPLISNKICNR-DVYGGIISPMMLCAGYLTGAVDSCQGDGGPLVYCER 409
 Db 938 SPADILQZEDDVPLLSNEKQQQMPEYN-ITEMMMCGYEEGIDSQGDGGPLMCLEN 995
 Qy 410 RLWYKVGATSGFICCAEVNKGPGVYTRYTSFLDWI 443
 Db 996 NRWLLAGVTSFGQCALPRPGVYARVPFTENT 1029

RESULT 12
 HEPs MOUSE STANDARD; PRT; 436 AA.
 ID HEPs MOUSE ; Q9CW97; 1.
 AC 034553; Q9CW97; 1.
 DT 15-TUL-1998 (Rel. 36, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Serine protease hepsin (EC 3.4.21.-).
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] _
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Liver;
 RX MEDLINE=98056912; PubMed=9305459;
 RA Vu T.-K.H., Liu R.W., Haakma C., Tomasek J.J., Howard E.W.;
 RT "Identification and cloning of the membrane-associated serine
 protease hepsin, from mouse preimplantation embryos.";
 JP J. Biol. Chem. 272:31315-3120(1997).
 RN [2] _
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=99339844; PubMed=10411637;
 RA Kawamura S., Kurachi S., Devashiki Y., Kurachi K.;
 RT "Complete nucleotide sequence, origin of isoform and functional
 characterization of the mouse hepsin gene.";
 RL Eur. J. Biochem. 262:755-764(1999).
 RN [3] _
 RP SEQUENCE FROM N.A. (ISOFORM 1);
 RC STRAIN=C57BL/6J; TISSUE=Kidney;

MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Komio H., Kiyosawa H., Kondo S., Yamamoto I.,
 RA Alzawa K., Izawa M., Nishii K., Matsuda H.A., Ashburner M., Bartalov S., Kasukawa T., Saito R.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Radotra K., Matsuda H.A., Ashburner T., Gissi C., King B., Kochiwa H., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Quackenbush J.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blaize J., Boiffelli D., Boujunga N., Garni P., de Bonaldo M.F.,
 RA Brownstein M.J., Built C., Fletcher C., Fujita M., Garibaldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Mazzarelli J., Montaudo P.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Montaudo P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,
 RA Wynshaw-Boris A., Toyooka K., Wang K.H., Weitz C., Whittraker C., Wilming L.,
 RA Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RA Brownstein M.J., Built C., Fletcher C., Fujita M., Garibaldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Montaudo P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,
 RA Wynshaw-Boris A., Toyooka K., Wang K.H., Weitz C., Whittraker C., Wilming L.,
 RA Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RA Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:655-656(2001).
 CC |- FUNCTION: Plays an essential role in cell growth and maintenance
 CC |- SUBCELLULAR LOCATION: Type II membrane protein.
 CC |- ALTERNATIVE PRODUCTS:
 CC |- Event=Alternative splicing; Named isoform=2;
 CC |- Name=1; Synonyms=1a;
 CC |- IsoId=035453-1; Sequence=Display;
 CC |- Note=Minor isoform;
 CC |- Name=2; Synonyms=2a;
 CC |- IsoId=03455-2; Sequence=Display;
 CC |- Note=Major isoform;
 CC |- SIMILARITY: Belongs to peptidase family SI.
 CC |- CAUTION: Ref. 3 sequence differs from that shown due to frameshifts in positions 155, 191 and 233.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@ebi-sib.ch).

CC |- AAB84241-1; ALT_FRAME.
 DR EMBL; AF030065; AAB84241-2; ALT_FRAME.
 DR EMBL; AR02694; BAB22289-2; ALT_FRAME.
 DR HSSP; P00763; 1DPO.
 DR MEROPS; S01-224 / -.
 DR MGD; MGI:1146620; Hpn.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR01254; Peptidase_SI.
 DR InterPro; IPR001314; Peptidase_SI.
 DR InterPro; IPR001190; Serin_receptor.
 DR Pfam; PF00089; trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPIN.
 DR SMART; SM00202; SR_1.
 DR SMART; SM00202; TRYSP; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SSR; 1.
 DR KW Hydrolase; Serine protease; Transmembrane; Signal-anchor; Alternative splicing.
 PT CHAIN 1 181
 PT DOMAIN 21 36
 PT TRANSMEM 37 63
 PT CHAIN 182 436
 PT DOMAIN 64 436
 PT DOMAIN 182 436
 PT ACT SITE 222 222
 PT ACT SITE 276 276

ACT SITE	372	CHARGE RELAY SYSTEM (BY SIMILARITY).	RT
FT DISULFID	172	INTERCHAIN (BY SIMILARITY).	RL submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
FT DISULFID	207	BY SIMILARITY.	RN [3]
FT DISULFID	341	BY SIMILARITY.	RP
FT DISULFID	368	BY SIMILARITY.	RC
FT CARBOHYD	131	N-JINKED (GLCNAC. . .) (POTENTIAL).	RX
FT VARSPLIC	25	Missing (in isoform 2).	MEDLINE=22388957; PubMed=12477937;
FT CONFLICT	85	/FRID=vSP000132.	RA
FT CONFLICT	204	L > F (IN REF. 2 AND 3).	Klausner R.D., Collins F.S., Wagner L., Shenmam C.M., Schuler G.D.,
FT CONFLICT	214	T > Y (IN REF. 3).	Altenschul S.F., Zeeberg B., Buetow K.H., Bhat N.K.,
FT CONFLICT	214	G > R (IN REF. 3).	Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Haich P.,
FT CONFLICT	229	ET > ET (IN REF. 3).	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
FT CONFLICT	264	P > L (IN REF. 3).	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
FT CONFLICT	281	H > N (IN REF. 3).	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Mullahy S.J., Abramson R.D., Mulhallan N.A., Peters G.J., Gunnarsson P.H., Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA
SQ SEQUENCE	436 AA;	46787 MW;	RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Query Match	27	Score 659.5; DB 1; Length 436;	Fatey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., RT
Best Local Similarity	38.6%	Pred. No. 3.1e-48;	RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Matches 116;	Conservative 49;	Mismatches 128;	RA Blakesley R.W., Touchman J.W., Green E.D., Dickerson M.C.,
Db 121 TAASWKTMCSDDWKGHAYANVACAOGLGFPSSYVSSDDNLRYVSLEQQFEEFVSID-----	173	CC	
Qy 88 TEGTWRLLCCRSRNRVAGLGCEEMGLFLALAHSELDVTAGANGTSGFCVDEGGIPLA 147		- - FUNCTION: Probable protease. Seems to be capable of activating	
Qy 174 -HLLPDDKTYTALHHSVYVTEBGASGHVTLQCTAGHRRGYSSRIVGMSLISQNPWQA 232		CC	
Db 148 QRLI--DVISVC-----DCPGRFLATCQDGFLRKLPYDTRIVGSCQDSLGRNEWQV 197		- - SUBCELLULAR LOCATION: Type II membrane protein (Potential).	
Qy 233 SLQFGQYHLCGGSVITPLWTTAAHCVYDYLPLK-----SMTIQVGVSLLDNPAHSL 286		CC	
Db 198 SLRVGTHLGGSLISGPDWLTAHC----FPERNRVLSRNEVFGAVAVARTSPHAVOLG 252		- - TISSUE SPECIFICITY: High levels in pancreatic, gastric, colorectal	
Qy 287 VEKITVHSKYKPKR-----LGNDITALMFLLAGPLTFENEMIQVCLPNSENFEDGKVWT 340		CC	
Db 253 VQAVIYGGXLPFRDPTIDENSNDTALVLUSSSLPLTEVITQPVCLPAQVQLVDGKVCT 312		- - SIMILARITY: Belongs to peptidase family S1.	
Qy 341 SGWKATEDGSDASPVLNHAAVPLISNKICNHRDVGIGLSPSMICAGTGTGGYDSCQGDS 400		CC	
Db 313 TGWGNTOFQYQQAMYLQEAVPNSNEVNSPDPYGNQNKPQDFCAGYFPEGGIDACQGDS 372		- - SIMILARITY: Contains 1 LDL-receptor class A domain.	
Qy 401 GGPLVNCQE---RRWIKLGATSPGIGCAEVNKEGVYTVTSFLDWIHEQME 448		CC	
Db 373 GGPPFYCEDSISGTSTSRWLRCLGIVSNGTGCAALKPGVYTVTDREWIFKAIAK 424		CC	
RESULT 13		CC	
ID TMS4_HUMAN	STANDARD;	PRT;	DR EMBL AF119224; AACF4526 1; -.
AC Q9NRZ4; Q9NZAS;			DR EMBL AF216312; AAP1436 1; -.
DT 16-OCT-2001 (Rel. 40, Created)			DR EMBL BC011703; AAHI1703 1; -.
DT 16-OCT-2001 (Rel. 40, Last sequence update)			DR HSSP P00763; 1DPO.
DE Transmembrane protease, serine 4 (EC 3.4.21.-) (Membrane-type serine			DR MEROPS SO1_034 1; -.
DE protease 2) (MP_SP2).			DR Newer HGNC:11878; TMPRSS4.
GN TMPRSS4 OR TMPRSS3.			DR NTM; 606565; -.
OS Homo sapiens (Human).			DR GO; GO:0016021; C:integral to membrane; NAS.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			DR GO; GO:0000252; F:serine-type endopeptidase activity; NAS.
OC Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.			DR GO; GO:00006508; P:proteinase and Peptidolysis; NAS.
OX NCBI_TaxID9606;			DR InterPro IPR000003; Cyb_Ser_trypsin.
RN [1]			DR InterPro IPR002742; LDL_receptor.
RP SEQUENCE FROM N.A.			DR InterPro IPR001254; Peptidase_S1.
RC TISSUE=Pancreatic carcinoma;			DR InterPro IPR001314; Peptidase_S1.
RX MEDLINE=20283276; PubMed=10825129;			DR InterPro IPR001190; Src_c receptor.
RA Willrap C., Haehnel S., Mueller-Pillatash F., Burghardt B.,			DR Pfam PF00057; ldl_recept_a_1.
RA Iwamura T., Ruthenburger M., Lerch M.M., Adler G., Gross T.M.,			DR Pfam PF00089; trypsin.
RT "A novel transmembrane serine protease (TMPRSS3) overexpressed in			DR PRINTS PR00722; CHYMOTRYPsin.
RT pancreatic cancer".			DR SMART SM00192; LDLalpha_1.
RT Cancer Res. 60:2602-2606 (2000).			DR SMART SM00202; SR; 1.
RN SEQUENCE FROM N.A.			DR SMART SM00022; TRYPSIN_SPC; 1.
RA Smeeleens S.S., Lorimer D.D., Wang E., Hou J., Linnevers C.;			DR PROSITE PS001209; LDURA_1; FALSE_NEG.
RT "MT-SP2, a novel type II membrane serine protease expressed in			DR PROSITE PS000420; SRCB_1; FALSE_NEG.
RT trachea, colon, and small intestine: identification, cloning, and			DR PROSITE PS551287; SRCK_2; 1.
RT			DR PROSITE PS55240; TRYPSIN_DOM; 1.
RA			DR PROSITE PS00134; TRYPSIN_HIS; 1.
RA Hydrolase; Serine protease; Transmembrane; Signal-anchor.			DR PROSITE PS00135; TRYPSIN_SER; 1.

FT DOMAIN	1	32	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	33	53	SIGNAL ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT DOMAIN	54	437	EXTRACELLULAR (POTENTIAL).
FT DOMAIN	61	93	LDL-RECEPTOR CLASS A.
FT DOMAIN	94	204	SRCR.
FT DOMAIN	205	437	SERINE PROTEASE.
FT ACT-SITE	245	245	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT-SITE	290	290	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT-SITE	387	387	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT SITE	204	205	CLEAVAGE (POTENTIAL).
FT DISULFID	64	83	BY SIMILARITY.
FT DISULFID	77	92	BY SIMILARITY.
FT DISULFID	127	183	BY SIMILARITY.
FT DISULFID	140	193	BY SIMILARITY.
FT DISULFID	196	310	BY SIMILARITY.
FT DISULFID	230	246	BY SIMILARITY.
FT DISULFID	356	372	BY SIMILARITY.
FT DISULFID	383	410	BY SIMILARITY.
FT CARBOHYD	130	130	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	178	178	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT	1	31	MLOQDPDSQQPLNSLYKPLRKRPIRMETFRK -> MSNPQPA
FT CONFLICT	31	31	NPSPSPRPBES (IN REF 2).
SEQ SEQUENCE	437 AA;	48204 MW;	351B2FD4A8657B12 CR64;
Query Match	26.9%	Score 658;	DB 1; Length 437;
Best Local Similarity	35.7%	Prd. No. 4.1e-4;	
Matches	158;	Conservative	75; Mismatches 146; Indels 64; Gaps 18;
Qy	44	LPLKFPIVIGITALILALA-----IGLIGHFDCSGKYRCRSSFKC---IELIAR--	91
Db	24	IPMETERWKPIPTIALSLASITIVVILKIVLD---KY----YFLQGPHLFPRKQL	76
Qy	92	CDGVSDCKGEDEVRC-----VRGGONAVLQVFTA--SWKTMCSDDWKGHYA	138
Db	77	CDGELDCPAGEDBEHCYRSFPEGPAPAVRLSDRSTLQLVLDATGNWSACDNFTEAL	136
Qy	139	NVACQOLGPSPSYSSDNLRVSSLEGOFREFEVSIDHILPPDKTALTHSVTVREG--CA	195
Db	137	ETARQOMGSS-----KPTFAVEISGPQDLDVETTENSOELMRMNSSGPCL	184
Qy	196	SGHVYTLOCTACGERRGYSRIVGNGMSLQWQASLQFOQYHLCGGSVITPLWHTIA	255
Db	185	SGSLVSLHACAG-KSLKTPRVGGEAVSDSVWQVIQDQHQVCGGSIIDPHWHLTA	243
Qy	256	AHCV--YDLYLPKPSWTQGVLVSLDNAPSHLVEKIV--YHSKXKPKRLGNIDLMK	309
Db	244	AHCPRKHTDVF--NWKVAGSDKL--GFPSLAVAKLIIIEFNPMY-PK--DNDIALMK	295
Qy	310	LAGPITPNEMIOPVCLPNSSEENPDGKVWTSGWGT EDGGDASPVLNHAAPLNSKI	368
Db	296	LQFPPLTFSGVYRPLPFDDELTPTPWIGNGFTHGRMSDILLQASQVQDSTR	355
Qy	369	CNHRDVYGGTISPSMLCAGYLTDGYDSCGDSGGPLVQCCRRLWKLVKATSGIGCAEVN	428
Db	356	CNADDAYOGVETXKMCAGIPEGGYVDTCCQDGSQFLMTQSDQ-WHVGIVSNQYCGGGS	414
Qy	429	KPGVYTRVTSFLDWTHEQERDL	451
Db	415	TPGVYTKVSAVNNWVNAEL	437
Query Match	26.8%	Score 654.5;	DB 1; Length 416;
Best Local Similarity	35.3%	Pred. No. 7.7e-48;	
Matches	146;	Conservative	61; Mismatches 156; Indels 51; Gaps 10;
Qy	60	ILALAIAGLGLTHFDCSCKYRKSSFCIELIARDGVSDDCKDGEDEYRCVRGONGAVLQV	119
Db	17	VAAIYTGTLLFLTGIG---AASWAVTILR-----SDQEPLVYQVLSPGDSRLVIL	65
Qy	120	-FTAAASWKTMCSDDWKGHYANVACQLGFPSSVYSSDNLYAVSSLBQFREEFVSD-	173
Db	66	DKTEGGWRLLCSRNSMRVAGLGCPENGFLRALKHSELVTRAGNTSGFFCYCDEGGILP	125
Qy	174	--HJLDDDKTALHHHSVYREGCASGHVYTLQCTAAGRHYSSRIVGNGMSLISQWPW	230
Db	126	LAQRLL-----DCPRGRFLPATCQDGRRKLPVDRIVGQDSSIGRWPW	175

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 OC RN [1];
 RP SEQUENCE FROM N.A.
 RX TISSUE-liver
 RC MEDLINE-93305733; PubMed=8318546;
 RA Parley D., Raymond F., Nick H.,
 RT Cloning and sequence analysis of rat hepsin,
 RT protease;
 RL Biochim Biophys Acta 1173:350-352(1993).
 RT -!- FUNCTION: Plays an essential role in cell growth and maintenance
 CC of cell morphology.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC
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 CC
 CC EMBL; X070900; CA50256.1; -
 DR FIR; S33777; S33777.
 DR HSSP; P00763; 1DPO.
 DR MEROPS; S01_224;
 DR InterPro; IPR09003; Cys_Ser_trypsin.
 DR InterPro; IPR01254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR01150; Src1_receptor.
 DR Pfam; PF00089; trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00202; SR_1.
 DR SMART; SM00022; TRYSPC_1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR CHAIN (POTENTIAL). SERINE PROTEASE HEPSIN, NON-CATALYTIC CHAIN
 KW Hydrolase; Serine protease; transmembrane; Signal-anchor.
 FT CHAIN 1 161 SERINE PROTEASE HEPSIN, CATALYTIC CHAIN
 FT CHAIN 162 416 (POTENTIAL). SERINE PROTEASE HEPSIN, CATALYTIC CHAIN
 FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL). SIGNAL ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT TRANSMEM 17 43 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 44 416 SERINE PROTEASE.
 FT ACT SITE 202 202 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISUFD 236 256 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISUFD 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISUFD 152 276 INTERCHAIN (BY SIMILARITY).
 FT DISUFD 187 203 BY SIMILARITY.
 FT DISUFD 321 337 BY SIMILARITY.
 FT DISUFD 348 380 BY SIMILARITY.
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 416 AA; 44926 MW; E5A9F8PA9550180 CRC64;

RESULT 14
 HEPS RAT STANDARD;
 ID HEPS RAT
 AC Q05511; 01-FEB-1994 (Rel. 28, Created)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Serine protease hepsin (EC 3.4.21.-).
 GN Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Dy	231	QASLQFGQYHLCGGSVITPLWIIITAHCVYDLYPK-----SWTIQVGLVSSLIDNPAPS	284
Db	176	QSVRLRYDGTTHLCGGSLLSGdwIAAHIC-----FPEANRVLSRWRVAFAGAARTSPHAQV	230
Dy	285	HIVVKTLVPHSKTKPKR-----LGNDIAIMKILAGBLTIRNEIOPVCLPNSEENFPDGKV/C	338
Db	231	LGYQAVLYHGGLYLPRDETDIENDIALVHLLSSPLTBTQPVCLPAACQLTDGKVC	290
Dy	339	WTSGWGATEBDGDDASPVLNHAAPVLSNKINCHRDVYGGIISPSMILCAGYLTGVDSCCG	398
Db	291	TWVGWTQFYQGQAVLQEARVPIINECVNSPDPFGNQIKPKMFCAGYBEGGDACQG	350
Dy	399	DSGGGLPYCQER---RLWKLVYCATSGIGCAEVNPKPGVYTRTSFLDWIHQME	448
Db	351	DSGGFHVCEFDRTSGTSRATLKGPGYTYKVIDFRWIFQAIK	404

RESULT 15					
SEQUENCE	AC	STANDARD;	PRT;	1069 AA.	
P97435; ENTK_MOUSE					
F97435; ENTK_MOUSE					
01-NOV-1997 01-NOV-1997		Rel. 35, Created)			
01-NOV-1997 28-FEB-2003		(Rel. 35, Last sequence update) (Rel. 41, Last annotation update)			
ENTEROKINASE (EC 3.4.21.9) (ENTEROKINASE).					
PRSS7 OR ENTK.					
Mus musculus (Mouse)					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.					
NCBI_TAXID=10090;					
[1..]					
RN					
SEQUENCE FROM N.A.					
STRAIN=C57BL/6; TISSUE=Duodenum;					
MEDLINE=9149142; Pubmed=9186180;					
Yuan X., Zheng X., Lu D., Rubin D.C., Pung C.Y.M., Sadler J.B.; i					
"Structure of murine enterokinase (enteropeptidase) and expression in small intestine during development.";					
Am. J. Physiol. 274:G142-G149(1998).					
-!- FUNCTION: Responsible for initiating activation of pancreatic proenzyme proenzymes (trypsin, chymotrypsin and carboxypeptidase A). It catalyzes the conversion of trypsinogen to trypsin which in turn activates other proenzymes including chymotrypsinogen, procarboxypeptidases, and proelastases (By similarity).					
-!- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys- -Leu-7 bond in trypsinogen.					
-!- SUBUNIT: Heterodimer of a catalytic (light) chain and a multidomain (heavy) chain linked by a disulfide bond (By similarity).					
CC					
-!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).					
-!- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS CLEAVED BY A TRYPSIN-LIKE PROTEASE (BY SIMILARITY).					
-!- SIMILARITY: Belongs to Peptidase Family S1.					
-!- SIMILARITY: Contains 2 CUB domains.					
-!- SIMILARITY: Contains 1 LDL-receptor class A domains.					
-!- SIMILARITY: Contains 1 MAM domain.					
-!- SIMILARITY: Contains 1 SEA domain.					
-!- SIMILARITY: Contains 1 SRCR domain.					
CC					
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EMBL: U73378; AAB3317.1; -
HSRP: Q07954; 1CR8.
MEROPS: S01-156; -
MGD: MGT:1197523; Press 7.
InterPro: IPR000859; CYS Ser trypsin.
InterPro: IPR000003; CYS Ser trypsin.

Query Match 26.6%; Score 651; DB 1; Length 1069;
 Best Local Similarity 37.4%; Preq. No. 4 .e-4;
 Matches 151; Conservatve 65; Mismatches 142; Indels 46; Gaps 17;

Qy 67 LGIHPDC-SGKYRGRSSFKCIELTARCDGSKDGDEYCRV--VGONAVLQVFT 121
 Db 682 LGIPEPCQDDEFQCKDG-NCIPGLNLCDSYPHCRGDSDEASCYRFNGLVQFN 1
 Qy 122 AASPRTMCCDDWKRHYANACQIGFPSPVSSDNLRVSLEQFREBVSIDHLLDDKV 181
 Qy 741 HSIWHIACLENWTTQISNEVCHLIGLS--ANSSMPISSTGG--GFVRVNYQ----- 788
 Qy 182 TALEHSVYREG--CASGHVVTLQCT--AGHBR--GYSRRIVGGNMISSQWPWQAST 234
 Db 789 -APNGSLITTPSLOQSDPQLLLOCNHSCEGEKVTQKVSPKVGGDAQAGAWPWTVAL 847
 Qy 235 QFGQYH-----LGCGSVITPLWITTAHAHCYDLYL-PKSWTIOVGL--VSLLDNP-A 282
 Db 848 ----YHRDSTDRLUCGASLVSQDWLVAHCVRRNLDPTRTAVLGHMOSNLSPQV 903
 Qy 283 PSHLVKEVITYHSCKYKPKRUGNDTALMKLAGPLTFENMIPQYCLPNSEENFPGKVWMTSG 342
 Db 904 VRRVVDQITINPHYDERRVNDAMMHIEFKVNTYTDYQPICLPEENQITFGRITCSIA 963
 Qy 343 WGATE-DGGDASPVLNHAAPLISNKICNR-DVGGIISPMLCAGYITGGVDSOGDS 400
 Db 964 WGYDKINAGSTVDVILKEAUVPLISNEKCOQQLBEYN--ITESNICAGYEGSIDSQGDS 1021
 Qy 401 GGPLVYCQERLWKGATSPGIGCAEVNPQGVYTRVTSFLDWH 444
 Db 1022 GGPLMCQENRWFVGVTSFGVQCALPNPQGVYTRVSQFIETH 1065

Search completed: May 5, 2004, 15:47:20
 Job time : 19 secs

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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:40:30 ; Search time 60 Seconds (without alignment)

Title: US-09-846-512-2

Perfect score: 2443

Sequence: 1 MGENDPPAVEAPFSSRSLFG.....TRVTSFLDWTHEQMERDLKT 453

Scoring table: BL2SUSM62

Gapext 0.5

Searched: 1566107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: GeneseqP1980s:*
2: GeneseqP1990s:*
3: GeneseqP2000s:*
4: GeneseqP2001s:*
5: GeneseqP2002s:*
6: GeneseqP2003s:*
7: GeneseqP2003bs:*
8: GeneseqP2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution:

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2443	100.0	453	4 AAU29055	Aau29055 Human PRO
2	2443	100.0	453	4 AAB06935	Aae06935 Human mem
3	2443	100.0	453	5 AAO18402	Aao18402 Human ser
4	2443	100.0	453	5 ABJ05565	Abj05565 Breast ca
5	2443	100.0	453	5 ABB3120	Aab3120 Human TRY
6	2443	100.0	453	6 ABU58431	Abu58431 Human PRO
7	2443	100.0	453	6 ABU87979	Abu87979 Novel hum
8	2443	100.0	453	6 ABU84294	Abu84294 Human sec
9	2443	100.0	453	6 ABR66168	Abr66168 Human sec
10	2443	100.0	453	6 ABR65558	Abr65558 Human sec
11	2443	100.0	453	6 ABU9498	Abu9498 Human sec
12	2443	100.0	453	6 ABU82737	Abu82737 Human PRO
13	2443	100.0	453	6 ABU89858	Abu89858 Novel hum
14	2443	100.0	453	6 ABR58549	Abr58549 Human can
15	2443	100.0	453	6 ABR68107	Abr68107 Human sec
16	2443	100.0	453	6 ABU96160	Abu96160 Novel hum
17	2443	100.0	453	6 ABU92591	Abu92591 Human sec
18	2443	100.0	453	6 ABU08668	Abu08668 Human sec
19	2443	100.0	453	6 ABP02720	Abp02720 Human sec
20	2443	100.0	453	6 ABR74874	Abr74874 Human sec
21	2443	100.0	453	6 ABR94636	Abr94636 Human sec
22	2443	100.0	453	6 ABQ25196	Abq25196 Novel hum
23	2443	100.0	453	6 ABU85609	Abu85609 Human PRO
24	2443	100.0	453	6 ABU98769	Abu98769 Novel hum
25	2443	100.0	453	6 ABU97984	Abu97984 Novel hum

ALIGNMENTS

RESULT 1
ID AAU29055 standard; protein; 453 AA.

AC AAU29055;

XX DT 18-DEC-2001 (first entry)

DE Human PRO polypeptide sequence #32

XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX OS Homo sapiens.

XX PN WO200168848-A2.

XX PD 20-SEP-2001.

XX PF 28-FEB-2001; 20001WO-US0005620.

XX PR 01-MAR-2000; 20000WO-US0005601.

PR 02-MAR-2000; 20000WO-US0005841.

PR 03-MAR-2000; 20000US-0187202P.

PR 06-MAR-2000; 20000US-0186988P.

PR 14-MAR-2000; 20000US-0189330P.

PR 14-MAR-2000; 20000US-0189322P.

PR 15-MAR-2000; 20000WO-US0005884.

PR 21-MAR-2000; 20000US-0190828P.

PR 21-MAR-2000; 20000US-0191007P.

PR 21-MAR-2000; 20000US-0191048P.

PR 21-MAR-2000; 20000US-0191314P.

PR 28-MAR-2000; 20000US-0192655P.

PR 29-MAR-2000; 20000US-0193022P.

PR 29-MAR-2000; 20000US-0193033P.

PR 30-MAR-2000; 20000WO-US0008439.

PR 04-APR-2000; 20000US-0194440P.

PR 04-APR-2000; 20000US-0194641P.

PR 11-APR-2000; 20000US-0195975P.

PR 11-APR-2000; 20000US-0196000P.

PR 11-APR-2000; 20000US-0196187P.

PR 11-APR-2000; 20000US-0196690P.

PR 11-APR-2000; 20000US-0196820P.

PR 18-APR-2000; 20000US-0198121P.

PR 25-APR-2000; 20000US-0199397P.

PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-JUN-2000; 2000HO-US013765.
 PR 22-MAY-2000; 2000HO-US014042.
 PR 30-MAY-2000; 2000HO-US014941.
 PR 02-JUN-2000; 2000HO-US015264.
 PR 05-JUN-2000; 2000HO-US015282.
 PR 28-AUG-2000; 2000HO-US020710.
 PR 22-AUG-2000; 2000HO-US020748.
 PR 24-AUG-2000; 2000HO-US022332.
 PR 08-NOV-2000; 2000HO-US030952.
 PR 01-DEC-2000; 2000HO-US032678.
 PR 20-DEC-2000; 2000HO-US034956.
 XX (GUTH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Godowski PJ, Gurney AL;
 Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-602746/58.
 DR N-PDB; AAS4956.
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 presence of tumors, such as prostate and breast tumors, in mammals and to
 screen for modulators of the compounds.
 PS Claim 11; Fig 64; 774pp; English.
 XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 detect the presence of a tumour in a mammal by comparing the level of
 expression of a PRO polypeptide in a test sample of cells from the animal
 and a control sample of normal cells, whereby a higher level of
 expression in the test sample indicates the presence of a tumour in the
 mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 and rabbits but are preferably human. The polypeptides can be used to
 stimulate tumour necrosis factor (TNF) alpha release from human blood,
 when contacted with it. A specific polypeptide can be used to stimulate
 the proliferation or differentiation of chondrocyte cells. The PRO
 proteins can be used to determine the presence of tumours and also
 susceptibility to tumour development, particularly adrenal, lung, colon,
 breast, prostate, rectal, cervical, or liver tumours, in mammalian
 subjects. The oligonucleotide probes specific for the PRO nucleic acids
 can be used for genetic analysis of individuals with genetic disorders
 XX Sequence 453 AA.
 XX Query Match 100.0%; Score 2443; DB 4; Length 453;
 Best Local Similarity 100.0%; Pred. No. 3 8e-18;
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGENDPPAVDAPPFRSPLIFGLDDLKISPAVADAAQAOILSLPLKPEPITIVIGIALL 60
 DB 1 MGENDPAAVDFPSRSPFLIFGLDDLKISPAVADAAQAOILSLPLKPEPITIVIGIALL 60
 QY 61 LALAIGLGHFDGSKRYCRSSFSKCIELAARCDSVSDCDGEDEYRCVRGGGNANIVQVF 120
 DB 61 LALAIGLGHFDGSKRYCRSSFSKCIELAARCDSVSDCDGEDEYRCVRGGGNANIVQVF 120
 QY 121 TAASWKTMCSDDWKGHAYNAYACAQLGFPSVYSSDMLRVSSLEGOFREEVTSIDHLPPDK 180
 DB 121 TAASWKTMCSDDWKGHAYNAYACAQLGFPSVYSSDMLRVSSLEGOFREEVTSIDHLPPDK 180
 QY 181 VITALHEHSVYVREGCAGHVTLQCTAGHRRGSSRIVEGANMSLLSQWMSLQFQCYH 240
 DB 181 VITALHEHSVYVREGCAGHVTLQCTAGHRRGSSRIVEGANMSLLSQWMSLQFQCYH 240
 QY 241 LGGSVYITPMLWITAAHCYDLYLPLKSWTIQLGVLSLLDNPAHSLVKEIVTHSKYKFR 300
 DB 241 LGGSVYITPMLWITAAHCYDLYLPLKSWTIQLGVLSLLDNPAHSLVKEIVTHSKYKFR 300
 QY 301 LGNDIALMKGLAGPLTNEMTIQPVCLPNSBENFPDGKVWTSGWGATEDGGDAEPVLNHA 360

Db 301 LGNDIALMKGLAGPLTNEMTIQPVCLPNSBENFPDGKVWTSGWGATEDGGDAEPVLNHA 360
 Qy 361 VPLISNKICNHDRYDYGITSPSMLCAGLITGGDSCQCDSGGPLVCCERRLMKLVGATSF 420
 Db 361 VPLISNKICNHDRYDYGITSPSMLCAGLITGGDSCQCDSGGPLVCCERRLMKLVGATSF 420
 Qy 421 GIGCAEVNKGFGVTPRTVSFLDWMHQMRDLKT 453
 Db 421 GIGCAEVNKGFGVTPRTVSFLDWMHQMRDLKT 453

RESULT 2
 AAE06935 standard; protein; 453 AA.
 ID AAE06935
 XX
 AC AAE06935;
 XX
 DT 16-OCT-2001 (first entry)
 DE Human membrane-type serine protease (MTSP) 6.
 XX
 KW transmembrane serine protease; membrane-type serine protease;
 MTSP; protease domain; neoplastic disease; tumour; cancer; cytosolic;
 lung carcinoma; colon adenocarcinoma; ovarian carcinoma; gene therapy.
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 48 .68 FT Domain
 /label= Transmembrane_domain
 72 .108 FT Domain
 /label= LDL receptor domain class a"
 /note= "LDL receptor domain class a"
 FT Domain
 FT Domain
 /label= SR domain
 /note= "Scavenger receptor Cys-rich domain"
 216 .435 FT Domain
 /note= "Trypsin-like serine protease domain"
 FT Cleavage-site
 FT Domains
 216 .217 FT
 /label= Protease_domain
 FT Misc-difference 324
 /note= "Unpaired cysteine"
 XX
 WO200157194-A2.

XX
 FD 09-AUG-2001.
 XX
 FF 02-FEB-2001; 2001WO-US003471.
 XX
 PR 03-FEB-2000; 2000US-017982P.
 PR 18-FEB-2000; 2000US-018542P.
 PR 22-JUN-2000; 2000US-0213124P.
 PR 08-SEP-2000; 2000US-00651986.
 PR 22-SEP-2000; 2000US-0234840P.
 XX
 PA (CORVAS INT INC.
 XX
 PA Madison EL, Ong EO, Yeh J;
 XX
 DR WPI; 2001-488877/53.
 DR N-PSDB; AAB13118.
 XX
 PT Novel single chain polypeptide comprising protease domain of type-II
 membrane-type serine protease or its catalytically active portion useful
 for treating and preventing cancer and tumor.
 XX
 PS Claim 128; Page 214-215; 256pp; English.
 XX
 CC The invention relates to transmembrane serine proteases and their
 corresponding nucleotides and the protease domain of a type-II membrane-

us-09-846-512-2.rag

PR	11-DEC-1997;	97US-0069335P.	PR	19-JUN-1998;	98US-0089952P.
PR	12-DEC-1997;	97US-0069428P.	PR	22-JUN-1998;	98US-009026P.
PR	17-DEC-1997;	97US-0069870P.	PR	22-JUN-1998;	98US-0090232P.
PR	18-DEC-1997;	97US-0068017P.	PR	22-JUN-1998;	98US-0090254P.
PR	10-MAR-1998;	98US-0077450P.	PR	24-JUN-1998;	98US-0090420P.
PR	11-MAR-1998;	98US-0077632P.	PR	24-JUN-1998;	98US-0090432P.
PR	11-MAR-1998;	98US-0077649P.	PR	24-JUN-1998;	98US-0090444P.
PR	20-MAR-1998;	98US-0078888P.	PR	24-JUN-1998;	98US-0090461P.
PR	20-MAR-1998;	98US-0078939P.	PR	24-JUN-1998;	98US-0090532P.
PR	27-MAR-1998;	98US-0079664P.	PR	24-JUN-1998;	98US-0091540P.
PR	27-MAR-1998;	98US-0079788P.	PR	25-JUN-1998;	98US-0090676P.
PR	31-MAR-1998;	98US-0081010P.	PR	25-JUN-1998;	98US-0090678P.
PR	31-MAR-1998;	98US-0080194P.	PR	25-JUN-1998;	98US-0090688P.
PR	01-APR-1998;	98US-0080327P.	PR	25-JUN-1998;	98US-0090690P.
PR	01-APR-1998;	98US-0080333P.	PR	25-JUN-1998;	98US-0090694P.
PR	08-APR-1998;	98US-0081049P.	PR	25-JUN-1998;	98US-0090695P.
PR	08-APR-1998;	98US-00811070P.	PR	25-JUN-1998;	98US-0090696P.
PR	09-APR-1998;	98US-0081195P.	PR	26-JUN-1998;	98US-009105413.
PR	15-APR-1998;	98US-0081380P.	PR	26-JUN-1998;	98US-00910862P.
PR	21-APR-1998;	98US-0082033P.	PR	26-JUN-1998;	98US-0091090P.
PR	21-APR-1998;	98US-0082568P.	PR	26-JUN-1998;	98US-0091094P.
PR	22-APR-1998;	98US-0082569P.	PR	26-JUN-1998;	98US-0091101P.
PR	22-APR-1998;	98US-0082704P.	PR	01-JUL-1998;	98US-00911359P.
PR	22-APR-1998;	98US-0082797P.	PR	01-JUL-1998;	98US-00911544P.
PR	28-APR-1998;	98US-0083322P.	PR	02-JUL-1998;	98US-00911747P.
PR	29-APR-1998;	98US-0083495P.	PR	02-JUL-1998;	98US-0091186P.
PR	29-APR-1998;	98US-0083496P.	PR	02-JUL-1998;	98US-0091226P.
PR	29-APR-1998;	98US-0083499P.	PR	02-JUL-1998;	98US-009128P.
PR	05-MAY-1998;	98US-0083559P.	PR	02-JUL-1998;	98US-009132P.
PR	05-MAY-1998;	98US-0084366P.	PR	01-AUG-1998;	98US-0094006P.
PR	06-MAY-1998;	98US-0084414P.	PR	04-AUG-1998;	98US-0094282P.
PR	07-MAY-1998;	98US-0084639P.	PR	10-AUG-1998;	98US-0094698P.
PR	07-MAY-1998;	98US-0084640P.	PR	10-AUG-1998;	98US-0094699P.
PR	15-MAY-1998;	98US-0084643P.	PR	17-AUG-1998;	98US-0094657P.
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PR	15-MAY-1998;	98US-0085858P.	PR	24-AUG-1998;	98US-0094867P.
PR	15-MAY-1998;	98US-0085982P.	PR	17-AUG-1998;	98US-0094891P.
PR	15-MAY-1998;	98US-0085100P.	PR	17-AUG-1998;	98US-0094897P.
PR	18-MAY-1998;	98US-0086023P.	PR	18-AUG-1998;	98US-0094949P.
PR	22-MAY-1998;	98US-0086392P.	PR	18-AUG-1998;	98US-0094959P.
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PR	04-JUN-1998;	98US-0088015P.	PR	26-AUG-1998;	98US-0097152P.
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PR	28-NAY-1998;	98US-0087208P.	PR	26-AUG-1998;	98US-0097198P.
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PR	05-JUN-1998;	98US-0088022P.	PR	02-SEP-1998;	98US-0097198P.
PR	05-JUN-1998;	98US-0088052P.	PR	02-SEP-1998;	98US-0097198P.
PR	04-JUN-1998;	98US-0088128P.	PR	09-SEP-1998;	98US-0099014P.
PR	05-JUN-1998;	98US-0088210P.	PR	01-SEP-1998;	98US-0098116P.
PR	04-JUN-1998;	98US-0088170P.	PR	01-SEP-1998;	98US-0098170P.
PR	09-SEP-1998;	98US-0088033P.	PR	10-SEP-1998;	98US-009803P.
PR	04-JUN-1998;	98US-0088130P.	PR	02-SEP-1998;	98US-009821P.
PR	05-JUN-1998;	98US-0088167P.	PR	02-SEP-1998;	98US-009843P.
PR	05-JUN-1998;	98US-0088202P.	PR	09-SEP-1998;	98US-009902P.
PR	10-JUN-1998;	98US-0088210P.	PR	16-SEP-1998;	98US-0100644P.
PR	05-JUN-1998;	98US-0088170P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088242P.	PR	16-SEP-1998;	98WO-US19330.
PR	10-JUN-1998;	98US-0088310P.	PR	17-SEP-1998;	98US-010383P.
PR	11-JUN-1998;	98US-008826P.	PR	17-SEP-1998;	98US-010384P.
PR	10-JUN-1998;	98US-0088167P.	PR	17-SEP-1998;	98US-010388P.
PR	11-JUN-1998;	98US-0088722P.	PR	17-SEP-1998;	98US-010389P.
PR	11-JUN-1998;	98US-0088738P.	PR	17-SEP-1998;	98US-010390P.
PR	11-JUN-1998;	98US-0088840P.	PR	18-SEP-1998;	98US-010394P.
PR	10-JUN-1998;	98US-0088811P.	PR	18-SEP-1998;	98US-0104104P.
PR	12-JUN-1998;	98US-0088817P.	PR	18-SEP-1998;	98US-0104168P.
PR	12-JUN-1998;	98US-0088815P.	PR	18-SEP-1998;	98US-0104171P.
PR	16-JUN-1998;	98US-0088826P.	PR	23-SEP-1998;	98US-0104172P.
PR	16-JUN-1998;	98US-0088861P.	PR	23-SEP-1998;	98US-0104173P.
PR	16-JUN-1998;	98US-0088863P.	PR	23-SEP-1998;	98US-0104175P.
PR	17-JUN-1998;	98US-0088876P.	PR	23-SEP-1998;	98US-0104177P.
PR	17-JUN-1998;	98US-0088881P.	PR	24-SEP-1998;	98US-0104178P.
PR	17-JUN-1998;	98US-0088900P.	PR	24-SEP-1998;	98US-0104179P.
PR	18-JUN-1998;	98US-0088908P.	PR	24-SEP-1998;	98US-0104179P.

PN	US2003032127-A1.
XX	24-SEP-1998;
PR	9B05-011739P;
PR	9B05-011743P;
PR	24-SEP-1998;
PR	9B05-011922P;
PR	25-SEP-1998;
PR	9B05-011786P;
PR	9B05-012207P;
PR	29-SEP-1998;
PR	9B05-012224P;
PR	29-SEP-1998;
PR	9B05-012330P;
PR	29-SEP-1998;
PR	9B05-012331P;
PR	30-SEP-1998;
PR	9B05-012487P;
PR	30-SEP-1998;
PR	9B05-012570P;
PR	30-SEP-1998;
PR	9B05-012671P;
PR	01-OCT-1998;
PR	9B05-012684P;
PR	01-OCT-1998;
PR	9B05-012687P;
PR	02-OCT-1998;
PR	9B05-012655P;
PR	06-OCT-1998;
PR	9B05-013258P;
PR	06-OCT-1998;
PR	9B05-013449P;
PR	07-OCT-1998;
PR	9B05-0168978.
Query Match	Score: 2443; DB: 6; Length: 453;
Best Local Similarity	100.0%
Matches	453; Conservative 0; N mismatches 0; Indels 0; Gaps 0;
Qy	1 MGENDPPAVAPPFERSLFLGDDDKISPIVAPDADAYAAQILSLPLKPEPPIIVIGITALI 60
Db	1 MGENDPPAVAPPFERSLFLGDDDKISPIVAPDADAYAAQILSLPLKPEPPIIVIGITALI 60
Qy	61 LALAGLGIHEDCGSKYRCRSSFKCIELIARCDGYSCKDGDIEDYRCYRGQNATLQVF 120
Db	61 LALAGLGIHEDCGSKYRCRSSFKCIELIARCDGYSCKDGDIEDYRCYRGQNATLQVF 120
Qy	121 TAASWKTMCSDDWKGHYANACQAGFPSTVSSDNLRVSSLEGQFREEVSTIDLLPDKX 180
Db	121 TAASWKTMCSDDWKGHYANACQAGFPSTVSSDNLRVSSLEGQFREEVSTIDLLPDKX 180
Qy	181 VTAHLHSVYREGCASGHVYLQCTAGHRRGYSSRIVGGNMSLISQWPQASHQFGYH 240
Db	181 VTAHLHSVYREGCASGHVYLQCTAGHRRGYSSRIVGGNMSLISQWPQASHQFGYH 240
Qy	241 LCGGSVITPLMIIATAHCYDLYLPKSMWLTQVGLYSSLNDNPAPSHLVKEVHSKYKPKR 300
Db	241 LCGGSVITPLMIIATAHCYDLYLPKSMWLTQVGLYSSLNDNPAPSHLVKEVHSKYKPKR 300
Qy	301 LGNDIALMKLAGPLFNEWTQPKWTCNSBNPDKVWTSGWATEDGDA5SVLNHA 360
Db	301 LGNDIALMKLAGPLTNEWMQPKVLPNSBNPDKVWTQVGLYSSLNDNPAPSHLVKEVHSKYKPKR 360
Qy	361 VPLISNKICNRDVYGGIIPSMSMLCAGYLTTGGVDSQCGDGGPLVCQERRLWKLGATSF 420
Db	361 VPLISNKICNRDVYGGIIPSMSMLCAGYLTTGGVDSQCGDGGPLVCQERRLWKLGATSF 420
Qy	421 GIGCAEYNKPGSTYTRUTSFLDWHQEMERDIKT 453
Db	421 GIGCAEYNKPGSTYTRUTSFLDWHQEMERDIKT 453
RESULT	7
ABU8779	ID ABU8779 standard; protein: 453 AA.
XX	07-JUL-2003 (First entry)
AC	ABU8779;
XX	Novel human secreted and transmembrane protein PRO382.
XX	Human; secreted and transmembrane protein; PRO; Gene therapy;
XX	tumour necrosis factor-alpha release; TNF-alpha release;
XX	chondrocyte proliferation; chondrocyte differentiation; tumour;
XX	adrenal tumour; lung tumour; colon tumour; breast tumour;
XX	prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX	Homo sapiens.

PR 05-JUN-1998; 98US-0088167P. PR 05-JUN-1998; 98US-0088222P. PR 05-JUN-1998; 98US-0088212P. PR 05-JUN-1998; 98US-0088655P. PR 05-JUN-1998; 98US-0088722P. PR 10-JUN-1998; 98US-0088718P. PR 10-JUN-1998; 98US-0088740P. PR 10-JUN-1998; 98US-008811P. PR 10-JUN-1998; 98US-0088824P. PR 10-JUN-1998; 98US-0088825P. PR 10-JUN-1998; 98US-0088825P. PR 11-JUN-1998; 98US-0088861P. PR 11-JUN-1998; 98US-0088863P. PR 11-JUN-1998; 98US-0088876P. PR 11-JUN-1998; 98US-0088909P. PR 12-JUN-1998; 98US-0088910P. PR 12-JUN-1998; 98US-0088910P. PR 16-JUN-1998; 98US-0088951P. PR 16-JUN-1998; 98US-0088951P. PR 17-JUN-1998; 98US-00889514P. PR 17-JUN-1998; 98US-00889538P. PR 17-JUN-1998; 98US-00889598P. PR 17-JUN-1998; 98US-00889651P. PR 18-JUN-1998; 98US-00889651P. PR 18-JUN-1998; 98US-00889652P. PR 22-JUN-1998; 98US-00890246P. PR 22-JUN-1998; 98US-00890254P. PR 24-JUN-1998; 98US-00890254P. PR 24-JUN-1998; 98US-00890429P. PR 24-JUN-1998; 98US-00890435P. PR 24-JUN-1998; 98US-00890442P. PR 24-JUN-1998; 98US-00890461P. PR 25-JUN-1998; 98US-00890535P. PR 25-JUN-1998; 98US-00890540P. PR 25-JUN-1998; 98US-00890676P. PR 25-JUN-1998; 98US-00890678P. PR 25-JUN-1998; 98US-00890689P. PR 25-JUN-1998; 98US-00891690P. PR 25-JUN-1998; 98US-00891694P. PR 25-JUN-1998; 98US-00890695P. PR 26-JUN-1998; 98US-00890695P. PR 26-JUN-1998; 98US-00890695P. PR 26-JUN-1998; 98US-00890695P. PR 26-JUN-1998; 98US-00890695P. PR 02-JUL-1998; 98US-0091478P. PR 02-JUL-1998; 98US-0091486P. PR 02-JUL-1998; 98US-0091626P. PR 02-JUL-1998; 98US-0091628P. PR 02-JUL-1998; 98US-0091632P. PR 04-AUG-1998; 98US-0094006P. PR 04-AUG-1998; 98US-0095282P. PR 10-AUG-1998; 98US-0095998P. PR 10-AUG-1998; 98US-0096897P. PR 18-AUG-1998; 98US-0096149P. PR 17-AUG-1998; 98US-0096359P. PR 17-AUG-1998; 98US-0096716P. PR 17-AUG-1998; 98US-0096867P. PR 17-AUG-1998; 98US-0096891P. PR 17-AUG-1998; 98US-009754P. PR 26-AUG-1998; 98US-0097955P. PR 26-AUG-1998; 98US-0097955P. PR 18-AUG-1998; 98US-0097971P. PR 18-AUG-1998; 98US-0098014P. PR 26-AUG-1998; 98US-0098716P. PR 01-SEP-1998; 98US-0098723P. PR 02-SEP-1998; 98US-0098803P. PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P. PR 09-SEP-1998; 98US-0099632P. PR 10-SEP-1998; 98US-0099711P. PR 10-SEP-1998; 98US-0099714P. PR 10-SEP-1998; 98US-0099763P. PR 10-SEP-1998; 98US-0099812P. PR 15-SEP-1998; 98US-0100389P. PR 16-SEP-1998; 98US-0100642P. PR 16-SEP-1998; 98US-0100645P. PR 16-SEP-1998; 98US-0101751P. PR 16-SEP-1998; 98US-05019330. PR 17-SEP-1998; 98US-0100683P. PR 17-SEP-1998; 98US-0100684P. PR 17-SEP-1998; 98US-0100911P. PR 17-SEP-1998; 98US-0100930P. PR 18-SEP-1998; 98US-01008449P. PR 18-SEP-1998; 98US-0101014P. PR 18-SEP-1998; 98US-0101068P. PR 18-SEP-1998; 98US-0101147P. PR 23-SEP-1998; 98US-01011472P. PR 23-SEP-1998; 98US-0101175P. PR 23-SEP-1998; 98US-0101177P. PR 24-SEP-1998; 98US-01011738P. PR 24-SEP-1998; 98US-01011739P. PR 24-SEP-1998; 98US-01011743P. PR 24-SEP-1998; 98US-01011922P. PR 25-SEP-1998; 98US-01011786P. PR 29-SEP-1998; 98US-010240P. PR 29-SEP-1998; 98US-0102330P. PR 29-SEP-1998; 98US-0102331P. PR 30-SEP-1998; 98US-010487P. PR 30-SEP-1998; 98US-0102570P. PR 30-SEP-1998; 98US-0102571P. PR 01-OCT-1998; 98US-010469P. PR 01-OCT-1998; 98US-0102687P. PR 02-OCT-1998; 98US-0102965P. PR 06-OCT-1998; 98US-0103158P.

Query Match 100.0%; Score 2443; DB 6; Length 453; Best Local Similarity 100.0%; Prod. No. 3. 8e-188; Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGENDPPAYEAPFSRSLFGLDDKLKISPVAPDADAVAAQILSLLPLKFPIITVIGIALI 60 Db 1 MGENDPPAYEAPFSRSLFGLDDKLKISPVAPDADAVAAQILSLLPLKFPIITVIGIALI 60

Qy 61 LALATGLGTHFDSCSKYRGRSSPFKCIELIARCGVSDCKDGEDEYRCVRGGONAVLQVF 120 Db 61 LALATGLGTHFDSCSKYRGRSSPFKCIELIARCGVSDCKDGEDEYRCVRGGONAVLQVF 120

Qy 121 TAASNTMCSDDWKGHYANVACAGLQFPYVSSDNLYSSLEGOFREEFVSYIDHLLPDDK 180 Db 121 TAASNTMCSDDWKGHYANVACAGLQFPYVSSDNLYSSLEGOFREEFVSYIDHLLPDDK 180

Qy 241 LGGGSTITPLMIIITAHCYDLYLPKSNTIQVGLVLDSLLNPAPHLVEKIVTISKYKPKR 300 Db 241 LGGGSTITPLMIIITAHCYDLYLPKSNTIQVGLVLDSLLNPAPHLVEKIVTISKYKPKR 300

Qy 361 VPLISKICICHFRDYYGIIISPSMLCAGYLTGGSQGSGPLVYCQERLWLVLGATSF 420 Db 361 VPLISKICICHFRDYYGIIISPSMLCAGYLTGGSQGSGPLVYCQERLWLVLGATSF 420

Qy 421 GIGCAEVNPKGVYTRVTSFLDIHQMERDLKT 453

Db 421 GIGCAEVNPKPGVYTRVTSSFLDWHQMERDLKT 453

RESULT 8
 ABU84294 standard; protein; 453 AA.
 XX AC ABU84294;
 XX DT 02-AUG-2003 (first entry)
 XX DE Human secreted/transmembrane protein (PRO) #32.
 XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
 tumour necrosis factor alpha; chondrocyte cell; tissue typing.
 XX KW Homo sapiens.
 XX PN US2003032112-A1.
 XX PD 13-FEB-2003.
 XX PF 21-JUN-2002; 2002US-00116756.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 17-OCT-1997; 97US-0062450P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 28-OCT-1997; 97US-0063540P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0063810P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0067712P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 17-DEC-1997; 97US-0070810P.
 PR 18-DEC-1997; 97US-0068017P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0080107P.
 PR 20-MAR-1998; 98US-0080372P.
 PR 20-MAR-1998; 98US-0080333P.
 PR 08-APR-1998; 98US-0081049P.
 PR 22-APR-1998; 98US-0082704P.
 PR 09-APR-1998; 98US-008115P.
 PR 31-MAR-1998; 98US-0081838P.
 PR 21-APR-1998; 98US-008194P.
 PR 01-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 08-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082797P.
 PR 28-APR-1998; 98US-008332P.
 PR 29-APR-1998; 98US-008349P.
 PR 29-APR-1998; 98US-008349P.
 PR 29-APR-1998; 98US-008355P.
 PR 05-MAY-1998; 98US-008436P.
 PR 06-MAY-1998; 98US-008441P.
 PR 07-MAY-1998; 98US-008463P.

PR 07-MAY-1998; 98US-0084640P.
 PR 07-MAY-1998; 98US-0084643P.
 PR 15-MAY-1998; 98US-008579P.
 PR 15-MAY-1998; 98US-008580P.
 PR 15-MAY-1998; 98US-008582P.
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 PR 22-MAY-1998; 98US-0086486P.
 PR 28-MAY-1998; 98US-008708P.
 PR 28-MAY-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-008825P.
 PR 04-JUN-1998; 98US-0088028P.
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 PR 04-JUN-1998; 98US-008817P.
 PR 09-JUN-1998; 98US-008855P.
 PR 10-JUN-1998; 98US-0088722P.
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 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088825P.
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 PR 11-JUN-1998; 98US-0088861P.
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 PR 12-JUN-1998; 98US-008900P.
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 PR 16-JUN-1998; 98US-0089512P.
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 PR 17-JUN-1998; 98US-0089518P.
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 PR 17-JUN-1998; 98US-0089539P.
 PR 18-JUN-1998; 98US-0089633P.
 PR 19-JUN-1998; 98US-0089922P.
 PR 22-JUN-1998; 98US-0090222P.
 PR 25-JUN-1998; 98US-0090234P.
 PR 22-JUN-1998; 98US-009042P.
 PR 24-JUN-1998; 98US-009044P.
 PR 24-JUN-1998; 98US-009046P.
 PR 24-JUN-1998; 98US-009053P.
 PR 24-JUN-1998; 98US-0090540P.
 PR 25-JUN-1998; 98US-0090678P.
 PR 25-JUN-1998; 98US-0090679P.
 PR 25-JUN-1998; 98US-0090680P.
 PR 26-JUN-1998; 98US-0090690P.
 PR 26-JUN-1998; 98US-0090694P.
 PR 01-JUL-1998; 98US-0091359P.
 PR 01-JUL-1998; 98US-0091544P.
 PR 02-JUL-1998; 98US-0091478P.
 PR 02-JUL-1998; 98US-0091486P.
 PR 02-JUL-1998; 98US-0091626P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 02-JUL-1998; 98US-0091632P.
 PR 24-JUL-1998; 98US-0091606P.
 PR 04-AUG-1998; 98US-0095282P.
 PR 10-AUG-1998; 98US-0095998P.

PR	10-AUG-1998;	98US-0096012P.	Db	121 TAASWKTMCDDWKGHYANVACAOGLFPSTYSSDNLRVSSLEGQFFEEFISDHLLPDK 180
PR	17-AUG-1998;	98US-0096757P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	17-AUG-1998;	98US-0096766P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	17-AUG-1998;	98US-0096891P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	17-AUG-1998;	98US-0096891P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	18-AUG-1998;	98US-0096940P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	18-AUG-1998;	98US-0096939P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	18-AUG-1998;	98US-0097022P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	26-AUG-1998;	98US-0097952P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	26-AUG-1998;	98US-0097954P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	26-AUG-1998;	98US-0097955P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	26-AUG-1998;	98US-0097971P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	26-AUG-1998;	98US-0097974P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	01-SEP-1998;	98US-0098014P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	01-SEP-1998;	98US-0098716P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	02-SEP-1998;	98US-0098723P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	02-SEP-1998;	98US-0098803P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	02-SEP-1998;	98US-0098821P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	09-SEP-1998;	98US-0098843P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	10-SEP-1998;	98US-0099602P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	10-SEP-1998;	98US-0099741P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	10-SEP-1998;	98US-0099754P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	10-SEP-1998;	98US-0099763P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	15-SEP-1998;	98US-0099812P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	16-SEP-1998;	98US-0100062P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	16-SEP-1998;	98US-0100066P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	16-SEP-1998;	98US-010151D.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	16-SEP-1998;	98US-0101933P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	17-SEP-1998;	98US-0100683P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	17-SEP-1998;	98US-0100684P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	17-SEP-1998;	98US-0100919P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	17-SEP-1998;	98US-0100930P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	18-SEP-1998;	98US-0100664P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	18-SEP-1998;	98US-0101751P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	18-SEP-1998;	98US-0101933P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	18-SEP-1998;	98US-0100683P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	18-SEP-1998;	98US-0100684P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	18-SEP-1998;	98US-0101472P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	18-SEP-1998;	98US-0101473P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	18-SEP-1998;	98US-0101475P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	24-SEP-1998;	98US-0101738P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	24-SEP-1998;	98US-0101739P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	24-SEP-1998;	98US-0101743P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	25-SEP-1998;	98US-0101922P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	25-SEP-1998;	98US-0101798P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	29-SEP-1998;	98US-0101477P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	29-SEP-1998;	98US-0102240P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	29-SEP-1998;	98US-0102331P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	30-SEP-1998;	98US-0102487P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	30-SEP-1998;	98US-0102570P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	01-OCT-1998;	98US-0102571P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	01-OCT-1998;	98US-0102684P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	02-OCT-1998;	98US-0102687P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	02-OCT-1998;	98US-0102965P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	06-OCT-1998;	98US-0103258P.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	06-OCT-1998;	98US-0103449P.	Qy	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
PR	07-OCT-1998;	98US-00168978.	Db	181 VTAHHHSYTVRECCASHEVVTIQLQCTAIGHRCYSSRIVGNNMSLISQWPQACISLQFGYH 240
Qy	Query Match Score 2443; DB 6; Length 453;			
Best Local Similarity 100.0%; Pred. No. 3 8e-18;				
Matches 453; Conservative 0; Mismatches 0; Gaps 0;				
1 MGENDPPAYEAPFSRSLPGLDLDKIKISPYAPDAAVAQILSILPLKEFPIIVIGIALI 60				
1 MGENDPPAVAPFSRSLPGLDLDKIKISPYAPDAAVAQILSILPLKEFPIIVIGIALI 60				
61 LALAIGLGHFDCSGKYRCRSSFKCTELARCDSGYSDCKDGEDBYRCVGGONAVIQYF 120				
61 LALAIGLGHFDCSGKYRCRSSFKCTELARCDSGYSDCKDGEDBYRCVGGONAVIQYF 120				
Qy	11-MAR-1998; 98US-0077332P.			

PR	11-MAR-1998;	98US-0077649P.	PR	24-JUN-1998;	98US-0090444P.
PR	20-MAR-1998;	98US-0078886P.	PR	24-JUN-1998;	98US-0090461P.
PR	20-MAR-1998;	98US-007939P.	PR	24-JUN-1998;	98US-0090535P.
PR	27-MAR-1998;	98US-0079661P.	PR	24-JUN-1998;	98US-0090540P.
PR	27-MAR-1998;	98US-0079786P.	PR	25-JUN-1998;	98US-0090676P.
PR	31-MAR-1998;	98US-0080107P.	PR	25-JUN-1998;	98US-0090678P.
PR	31-MAR-1998;	98US-0080194P.	PR	25-JUN-1998;	98US-0090688P.
PR	01-APR-1998;	98US-0080327P.	PR	25-JUN-1998;	98US-0090690P.
PR	01-APR-1998;	98US-0080333P.	PR	25-JUN-1998;	98US-0090694P.
PR	08-APR-1998;	98US-0081049P.	PR	25-JUN-1998;	98US-0090695P.
PR	08-APR-1998;	98US-0081070P.	PR	25-JUN-1998;	98US-0091696P.
PR	09-APR-1998;	98US-0081195P.	PR	26-JUN-1998;	98US-0091043.
PR	15-APR-1998;	98US-008118P.	PR	26-JUN-1998;	98US-0091062P.
PR	21-APR-1998;	98US-0082568P.	PR	26-JUN-1998;	98US-0091163P.
PR	21-APR-1998;	98US-0082569P.	PR	26-JUN-1998;	98US-0091169P.
PR	22-APR-1998;	98US-0082704P.	PR	01-JUL-1998;	98US-0091359P.
PR	22-APR-1998;	98US-0082797P.	PR	01-JUL-1998;	98US-0091447P.
PR	28-APR-1998;	98US-0083322P.	PR	02-JUL-1998;	98US-0091478P.
PR	29-APR-1998;	98US-0083495P.	PR	02-JUL-1998;	98US-0091486P.
PR	29-APR-1998;	98US-0083496P.	PR	02-JUL-1998;	98US-0091492P.
PR	29-APR-1998;	98US-0083499P.	PR	02-JUL-1998;	98US-0091498P.
PR	05-MAY-1998;	98US-0083559P.	PR	02-JUL-1998;	98US-0091632P.
PR	06-MAY-1998;	98US-0084366P.	PR	04-AUG-1998;	98US-0091782P.
PR	07-MAY-1998;	98US-0084639P.	PR	02-JUL-1998;	98US-0091846P.
PR	07-MAY-1998;	98US-0084640P.	PR	10-AUG-1998;	98US-0096012P.
PR	07-MAY-1998;	98US-0084643P.	PR	10-AUG-1998;	98US-0096017P.
PR	15-MAY-1998;	98US-008479P.	PR	17-AUG-1998;	98US-0096716P.
PR	15-MAY-1998;	98US-008479P.	PR	17-AUG-1998;	98US-0096806P.
PR	15-MAY-1998;	98US-008514P.	PR	17-AUG-1998;	98US-0096891P.
PR	18-MAY-1998;	98US-0086023P.	PR	17-AUG-1998;	98US-0096897P.
PR	22-MAY-1998;	98US-008632P.	PR	18-AUG-1998;	98US-0096949P.
PR	28-MAY-1998;	98US-0086486P.	PR	18-AUG-1998;	98US-0096959P.
PR	28-MAY-1998;	98US-0086580P.	PR	18-AUG-1998;	98US-0097022P.
PR	28-MAY-1998;	98US-0086582P.	PR	26-AUG-1998;	98US-009716P.
PR	02-JUN-1998;	98US-008700P.	PR	26-AUG-1998;	98US-009754P.
PR	03-JUN-1998;	98US-0087759P.	PR	26-AUG-1998;	98US-009755P.
PR	04-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-009774P.
PR	05-JUN-1998;	98US-0088025P.	PR	26-AUG-1998;	98US-0098014P.
PR	04-JUN-1998;	98US-0088028P.	PR	01-SEP-1998;	98US-009816P.
PR	04-JUN-1998;	98US-0088029P.	PR	01-SEP-1998;	98US-009823P.
PR	09-JUN-1998;	98US-0088032P.	PR	02-SEP-1998;	98US-009803P.
PR	10-JUN-1998;	98US-0088262P.	PR	02-SEP-1998;	98US-009821P.
PR	10-JUN-1998;	98US-0088167P.	PR	09-SEP-1998;	98US-009843P.
PR	10-JUN-1998;	98US-0088202P.	PR	09-SEP-1998;	98US-00985602P.
PR	05-JUN-1998;	98US-0088212P.	PR	10-SEP-1998;	98US-0098716P.
PR	05-JUN-1998;	98US-0088217P.	PR	10-SEP-1998;	98US-009954P.
PR	10-JUN-1998;	98US-0088242P.	PR	10-SEP-1998;	98US-009963P.
PR	10-JUN-1998;	98US-0088252P.	PR	10-SEP-1998;	98US-0100683P.
PR	16-JUN-1998;	98US-0088822P.	PR	17-SEP-1998;	98US-010088P.
PR	16-JUN-1998;	98US-0088838P.	PR	17-SEP-1998;	98US-0100919P.
PR	17-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100930P.
PR	17-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-0100949P.
PR	17-JUN-1998;	98US-0088871P.	PR	18-SEP-1998;	98US-0101144P.
PR	12-JUN-1998;	98US-0088910P.	PR	18-SEP-1998;	98US-0101148P.
PR	16-JUN-1998;	98US-0088912P.	PR	18-SEP-1998;	98US-0101168P.
PR	16-JUN-1998;	98US-0088867P.	PR	23-SEP-1998;	98US-0101471P.
PR	17-JUN-1998;	98US-0089338P.	PR	23-SEP-1998;	98US-0101472P.
PR	17-JUN-1998;	98US-0089398P.	PR	23-SEP-1998;	98US-0101475P.
PR	17-JUN-1998;	98US-0089552P.	PR	23-SEP-1998;	98US-0101477P.
PR	18-JUN-1998;	98US-0089408P.	PR	24-SEP-1998;	98US-0101478P.
PR	19-JUN-1998;	98US-0089522P.	PR	24-SEP-1998;	98US-0101479P.
PR	22-JUN-1998;	98US-0090246P.	PR	24-SEP-1998;	98US-0101443P.
PR	22-JUN-1998;	98US-009052P.	PR	24-SEP-1998;	98US-0101422P.
PR	24-JUN-1998;	98US-0090429P.	PR	29-SEP-1998;	98US-0101468P.
PR	24-JUN-1998;	98US-0090435P.	PR	29-SEP-1998;	98US-0102240P.

Query Match 100.0% ; Score 2443; DB 6; Length 453;
 Best Local Similarity 100.0% ; Pred. No. 3 ; 8e-188 ;
 Matches 453 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

1 MGENDPPAYEAPFSRSLSLGLDDLIKSPAPDADAAQIILSILPKFPIVIGITALI 60
 1 MGENDPPAYEAPFSRSLSLGLDDLIKSPAPDADAAQIILSILPKFPIVIGITALI 60

61 LALAGLIGHFDCCGKYRGRSSPCKIELIARCDGVSDCKDGEDEYRCVRVGQNAVLOVF 120
 61 LALAGLIGHFDCCGKYRGRSSPCKIELIARCDGVSDCKDGEDEYRCVRVGQNAVLOVF 120

121 TAASWKTMSDDWKGHYANAVACAOLGFPIVYSSDNLRVSLEQCFREFFVS DHLAPDK 180
 121 TAASWKTMSDDWKGHYANAVACAOLGFPIVYSSDNLRVSLEQCFREFFVS DHLAPDK 180

181 VITALHHSVTVREGCASHVTVLQCTACGERRGYSRITVGGNNMSLLSQWQASLQFGYH 240
 181 VITALHHSVTVREGCASHVTVLQCTACGERRGYSRITVGGNNMSLLSQWQASLQFGYH 240

241 LGCGSVITPLWITAHCYDLYLPKSNTWITQGVLSLDNPASHLTYEKIVTHSKYKPKR 300
 241 LGCGSVITPLWITAHCYDLYLPKSNTWITQGVLSLDNPASHLTYEKIVTHSKYKPKR 300

301 LGNDIALMCLAGPLTENEMIQPVCLPNSENENPDKVWTMSKGATEDGGDASPVLNHA 360
 301 LGNDIALMCLAGPLTENEMIQPVCLPNSENENPDKVWTMSKGATEDGGDASPVLNHA 360

361 VPLISNKICNRDYYGGIISPMECAQYITGGDSCQGDGPGLVCQERLWLVGATSF 420
 361 VPLISNKICNRDYYGGIISPMLCAGYLTG3TDSCQGSGLVCQERLWLVGATSF 420

421 GIGCAEVNPKGYVIRTSFLDWTHEQMEDLKT 453
 421 GIGCAEVNPKGYVIRTSFLDWTHEQMEDLKT 453

RESULT 10
 ABR5558 ID: ABR5558 standard; protein; 453 AA.
 XX Human secreted polypeptide PRO382, SEQ ID NO:64.

XX DE Human secreted polypeptide PRO382, SEQ ID NO:64.
 XX AC ABR5558;
 XX DT 05-AUG-2003 (first entry)
 XX DE Human secreted polypeptide PRO382, SEQ ID NO:64.
 XX AC ABR5558;
 XX DT 05-AUG-2003 (first entry)
 XX OS Homo sapiens.
 XX PN US2003036159-A1.
 XX PD 20-FEB-2003.
 XX PF 02-JUL-2002; 2002US-00188773.
 XX PR 18-SEP-1997; 97US-0059631P.
 XX PR 18-SEP-1997; 97US-0059266P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0053486P.
 PR 24-OCT-1997; 97US-0053120P.
 PR 24-OCT-1997; 97US-0053121P.
 PR 28-OCT-1997; 97US-0053540P.
 PR 28-OCT-1997; 97US-0053541P.
 PR 28-OCT-1997; 97US-0053544P.
 PR 28-OCT-1997; 97US-0053546P.
 PR 29-OCT-1997; 97US-005334P.
 PR 31-OCT-1997; 97US-005370P.
 PR 31-OCT-1997; 97US-006103P.
 PR 13-NOV-1997; 97US-0055311P.
 PR 21-NOV-1997; 97US-0065120P.
 PR 24-NOV-1997; 97US-0065466P.
 PR 27-NOV-1997; 97US-0065772P.
 PR 11-DEC-1997; 97US-0059335P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 17-DEC-1997; 97US-006970P.
 PR 18-DEC-1997; 97US-0068017P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077132P.
 PR 20-MAR-1998; 98US-0078886P.
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 PR 27-MAR-1998; 98US-00787964P.
 PR 27-MAR-1998; 98US-00787876P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080333P.
 PR 08-APR-1998; 98US-0081049P.
 PR 09-APR-1998; 98US-0081070P.
 PR 15-APR-1998; 98US-0081195P.
 PR 15-APR-1998; 98US-0081838P.
 PR 21-APR-1998; 98US-0082568P.
 PR 22-APR-1998; 98US-0082704P.
 PR 28-APR-1998; 98US-0083322P.
 PR 29-APR-1998; 98US-0083495P.
 PR 29-APR-1998; 98US-0084196P.
 PR 29-APR-1998; 98US-0083499P.
 PR 05-MAY-1998; 98US-0084366P.
 PR 06-MAY-1998; 98US-0084414P.
 PR 07-MAY-1998; 98US-0084639P.
 PR 07-MAY-1998; 98US-0084640P.
 PR 07-MAY-1998; 98US-0084643P.
 PR 15-MAY-1998; 98US-008579P.
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 PR 15-MAY-1998; 98US-008582P.
 PR 02-JUN-1998; 98US-0085100P.
 PR 03-JUN-1998; 98US-008727P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088028P.
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 PR 05-JUN-1998; 98US-0088302P.
 PR 05-JUN-1998; 98US-0088312P.
 PR 05-JUN-1998; 98US-0088317P.
 PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088722P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-00883140P.

XX Human secreted/transmembrane protein (PRO) #32.
DE Human; secreted and transmembrane Protein (PRO); TNF-alpha; tumour; gene therapy;
XX Human; secreted and transmembrane Protein (PRO); chondrocyte cell; tumour; gene therapy;
KW tumour necrosis factor alpha;
KW tissue typing.
XX Homo sapiens.
OS Homo sapiens.
XX US2003040070-A1.
XX PD 27-FEB-2003.
XX PP 27-JUN-2002; 2002US-00184627.
XX PR 28-MAY-1998; 98US-0087208P.
PR PR 02-JUN-1998; 98US-0087609P.
PR PR 02-JUN-1998; 98US-0087759P.
PR PR 03-JUN-1998; 98US-0087827P.
PR PR 04-JUN-1998; 98US-0088025P.
PR PR 04-JUN-1998; 98US-0088028P.
PR PR 04-JUN-1998; 98US-0088129P.
PR PR 04-JUN-1998; 98US-0088033P.
PR PR 04-JUN-1998; 98US-0088126P.
PR PR 05-JUN-1998; 98US-0088167P.
PR PR 05-JUN-1998; 98US-0088202P.
PR PR 05-JUN-1998; 98US-0088212P.
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PR PR 10-JUN-1998; 98US-0088722P.
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PR PR 10-JUN-1998; 98US-0088811P.
PR PR 10-JUN-1998; 98US-0088824P.
PR PR 10-JUN-1998; 98US-0088825P.
PR PR 10-JUN-1998; 98US-0088826P.
PR PR 11-JUN-1998; 98US-0088861P.
PR PR 11-JUN-1998; 98US-0088863P.
PR PR 11-JUN-1998; 98US-0088876P.
PR PR 12-JUN-1998; 98US-0088909P.
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PR PR 24-JUN-1998; 98US-0090535P.
PR PR 24-JUN-1998; 98US-0090540P.
PR PR 25-JUN-1998; 98US-0090676P.
PR PR 25-JUN-1998; 98US-0090779P.
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PR PR 25-JUN-1998; 98US-0091694P.
PR PR 25-JUN-1998; 98US-0091359P.
PR PR 01-JUL-1998; 98US-0091544P.
PR PR 02-JUL-1998; 98US-00105413.
PR PR 02-JUL-1998; 98US-0091662P.
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PR PR 17-AUG-1998; 98US-0096766P.
PR PR 17-AUG-1998; 98US-0096867P.
PR PR 17-AUG-1998; 98US-009891P.
PR PR 17-AUG-1998; 98US-0098917P.
PR PR 18-AUG-1998; 98US-0098949P.
PR PR 18-AUG-1998; 98US-0098959P.
PR PR 18-AUG-1998; 98US-0097022P.
PR PR 26-AUG-1998; 98US-0097952P.

PR	26-AUG-1998;	98US-0097954P.	Qy	301	LGNDIALMCLAGPLTFENEMIQPVCLPNSSENFDPGKIVCWTSGWATEPDGGDASPVLNHAA	360
PR	26-AUG-1998;	98US-0097971P.	Db	301	LGNDIALMCLAGPLTFENEMIQPVCLPNSSENFDPGKIVCWTSGGATEPDGGDASPVLNHAA	360
PR	26-AUG-1998;	98US-0097974P.	Qy	361	VPLISNKICNHRDVYGGTISPSMLCAGYLTCGDSDGGLVWCQERLINKLVLGVATSF	420
PR	01-SEP-1998;	98US-0098716P.	Db	361	VPLISNKICNHRDVYGGTISPSMLCAGYLTCGDSDGGLVWCQERLINKLVLGVATSF	420
PR	01-SEP-1998;	98US-0098723P.	Qy	361	VPLISNKICNHRDVYGGTISPSMLCAGYLTCGDSDGGLVWCQERLINKLVLGVATSF	420
PR	02-SEP-1998;	98US-0098801P.	Db	361	VPLISNKICNHRDVYGGTISPSMLCAGYLTCGDSDGGLVWCQERLINKLVLGVATSF	420
PR	02-SEP-1998;	98US-0098821P.	Qy	421	GIGCAEVNPKPGVYTRVTSPLDWIHEQMFRDLKT	453
PR	02-SEP-1998;	98US-0098843P.	Db	421	GIGCAEVNPKPGVYTRVTSPLDWIHEQMFRDLKT	453
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PR	10-SEP-1998;	98US-0099741P.				
PR	10-SEP-1998;	98US-0099742P.				
PR	10-SEP-1998;	98US-0099763P.				
PR	10-SEP-1998;	98US-0099812P.				
PR	15-SEP-1998;	98US-0100388P.				
PR	16-SEP-1998;	98US-0100662P.				
PR	16-SEP-1998;	98US-0101751P.				
PR	16-SEP-1998;	98USO-US19333P.				
PR	17-SEP-1998;	98US-0100683P.				
PR	17-SEP-1998;	98US-0100684P.				
PR	17-SEP-1998;	98US-0100919P.				
PR	17-SEP-1998;	98US-0100930P.				
PR	18-SEP-1998;	98US-0100849P.				
PR	18-SEP-1998;	98US-0101044P.				
PR	18-SEP-1998;	98US-0101068P.				
PR	23-SEP-1998;	98US-0101471P.				
PR	23-SEP-1998;	98US-0101472P.				
PR	23-SEP-1998;	98US-0101475P.				
PR	23-SEP-1998;	98US-0101477P.				
PR	24-SEP-1998;	98US-0101738P.				
PR	24-SEP-1998;	98US-0101739P.				
PR	24-SEP-1998;	98US-0101743P.				
PR	24-SEP-1998;	98US-0101922P.				
PR	25-SEP-1998;	98US-0101786P.				
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PR	29-SEP-1998;	98US-0102240P.				
PR	29-SEP-1998;	98US-0102310P.				
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PR	30-OCT-1998;	98US-0102487P.				
PR	30-OCT-1998;	98US-0102570P.				
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PR	01-OCT-1998;	98US-010684P.				
PR	01-OCT-1998;	98US-0102687P.				
PR	02-OCT-1998;	98US-0102955P.				
PR	06-OCT-1998;	98US-0103258P.				
PR	07-OCT-1998;	98US-0103449P.				
PR	07-OCT-1998;	98US-00169978.				
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Qy	1 LALAIGLIGHFDGSKYRGRSSPFCLIELARCQVDSDCKDGEDBEYRCYVGQNAYLF	120				
Db	1 LALAIGLIGHFDGSKYRGRSSPFCLIELARCQVDSDCKDGEDBEYRCYVGQNAYLF	120				
Qy	181 VTALEHSVTVREGGASGHVTQCTACGRRGYSSRIVGNNMSLLSQWPQASLQFGYH	240				
Db	181 VTALEHSVTVREGGASGHVTQCTACGRRGYSSRIVGNNMSLLSQWPQASLQFGYH	240				
Qy	121 TAASKMTMDDWKGHYANVACAQLGFPYVSSDNLRVSLQFREPPVS DHL L PDK	180				
Db	121 TAASKMTMDDWKGHYANVACAQLGFPYVSSDNLRVSLQFREPPVS DHL L PDK	180				
Qy	61 LALAIGLIGHFDGSKYRGRSSPFCLIELARCQVDSDCKDGEDBEYRCYVGQNAYLF	120				
Db	61 LALAIGLIGHFDGSKYRGRSSPFCLIELARCQVDSDCKDGEDBEYRCYVGQNAYLF	120				
Qy	181 VTALEHSVTVREGGASGHVTQCTACGRRGYSSRIVGNNMSLLSQWPQASLQFGYH	240				
Db	181 VTALEHSVTVREGGASGHVTQCTACGRRGYSSRIVGNNMSLLSQWPQASLQFGYH	240				
Qy	121 LCGGSVITPLWITDAHCVTDLYLPKSNTIQGLVSLUDNPASHLYEKIVTHSKYKPKR	300				
Db	121 LCGGSVITPLWITDAHCVTDLYLPKSNTIQGLVSLUDNPASHLYEKIVTHSKYKPKR	300				
Qy	181 VTALEHSVTVREGGASGHVTQCTACGRRGYSSRIVGNNMSLLSQWPQASLQFGYH	240				
Db	181 VTALEHSVTVREGGASGHVTQCTACGRRGYSSRIVGNNMSLLSQWPQASLQFGYH	240				
Qy	241 LCGGSVITPLWITDAHCVTDLYLPKSNTIQGLVSLUDNPASHLYEKIVTHSKYKPKR	300				
Db	241 LCGGSVITPLWITDAHCVTDLYLPKSNTIQGLVSLUDNPASHLYEKIVTHSKYKPKR	300				

PR	22-APR-1998;	98US-00882704P;	PR	01-JUL-1998;	98US-0091359P;
PR	22-APR-1998;	98US-0082797P;	PR	01-JUL-1998;	98US-0091544P;
PR	28-APR-1998;	98US-0083322P;	PR	02-JUL-1998;	98US-0091478P;
PR	29-APR-1998;	98US-00832495P;	PR	02-JUL-1998;	98US-0091486P;
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PR	03-JUN-1998;	98US-0087822P;	PR	26-AUG-1998;	98US-0097974P;
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PR	04-JUN-1998;	98US-0088028P;	PR	26-AUG-1998;	98US-009814P;
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PR	10-JUN-1998;	98US-0088722P;	PR	10-SEP-1998;	98US-0099812P;
PR	10-JUN-1998;	98US-0088738P;	PR	15-SEP-1998;	98US-0100388P;
PR	10-JUN-1998;	98US-0088740P;	PR	16-SEP-1998;	98US-0100662P;
PR	11-JUN-1998;	98US-0088811P;	PR	16-SEP-1998;	98US-0100664P;
PR	10-JUN-1998;	98US-0088244P;	PR	16-SEP-1998;	98US-0101751P;
PR	10-JUN-1998;	98US-0088825P;	PR	16-SEP-1998;	98NO-US019330;
PR	10-JUN-1998;	98US-0088826P;	PR	17-SEP-1998;	98US-0101683P;
PR	11-JUN-1998;	98US-0088861P;	PR	17-SEP-1998;	98US-0101684P;
PR	11-JUN-1998;	98US-0088863P;	PR	17-SEP-1998;	98US-0100919P;
PR	17-JUN-1998;	98US-0088876P;	PR	17-SEP-1998;	98US-0100930P;
PR	18-JUN-1998;	98US-0089090P;	PR	18-SEP-1998;	98US-0100949P;
PR	12-JUN-1998;	98US-0089105P;	PR	18-SEP-1998;	98US-0101014P;
PR	16-JUN-1998;	98US-0089512P;	PR	18-SEP-1998;	98US-0101068P;
PR	16-JUN-1998;	98US-0089514P;	PR	23-SEP-1998;	98US-0101471P;
PR	22-JUN-1998;	98US-0090252P;	PR	23-SEP-1998;	98US-0101472P;
PR	22-JUN-1998;	98US-0090254P;	PR	23-SEP-1998;	98US-0101475P;
PR	24-JUN-1998;	98US-0090429P;	PR	23-SEP-1998;	98US-0101477P;
PR	24-JUN-1998;	98US-0090435P;	PR	24-SEP-1998;	98US-0102240P;
PR	25-JUN-1998;	98US-0090676P;	PR	29-SEP-1998;	98US-0102240P;
PR	25-JUN-1998;	98US-0090678P;	PR	01-OCT-1998;	98US-0102684P;
PR	24-JUN-1998;	98US-0090444P;	PR	01-OCT-1998;	98US-0102330P;
PR	25-JUN-1998;	98US-0090690P;	PR	29-SEP-1998;	98US-0102687P;
PR	25-JUN-1998;	98US-0090694P;	PR	02-OCT-1998;	98US-0102965P;
PR	25-JUN-1998;	98US-0090695P;	PR	06-OCT-1998;	98US-0103258P;
PR	25-JUN-1998;	98US-0090696P;	PR	06-OCT-1998;	98US-0103449P;
PR	26-JUN-1998;	98US-00105413;	PR	07-OCT-1998;	98US-00168978;
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			Query Match	100.0%	Score 2443; DB 6;
			Best Local Similarity	100.0%;	Pred. No. 3.8e-188;

Matches	453;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MGENDPVAPFSSRSLRGLDDIKRISPVAPDADAVAGILSLLPLKFPIIVIGITALI	60						
Db	1	MGENDPVAPFSSRSLRGLDDIKRISPVAPDADAVAGILSLLPLKFPIIVIGITALI	60						
Qy	61	LALAIGLGHIFDCSGKRYCRSSPKCIELARCDGVSDCDCGEDEYRCVRGGONAVLQVF	120						
Db	61	LALAIGLGHIFDCSGKRYCRSSPKCIELARCDGVSDCDCGEDEYRCVRGGONAVLQVF	120						
Qy	121	TAASPKTMCDDWKRHYANVACAOLGFPPYVSSDNLRVSLGQFREEFVSDHLLPDK	180						
Db	121	TAASPKTMCDDWKRHYANVACAOLGFPPYVSSDNLRVSLGQFREEFVSDHLLPDK	180						
Qy	181	VITALHHSVYTRREGCASGHVYLLOCTACGRGRRGSSRRTIVCGNMSSLISQWPWQASLQFGCYH	240						
Db	181	VITALHHSVYTRREGCASGHVYLLOCTACGRGRRGSSRRTIVCGNMSSLISQWPWQASLQFGCYH	240						
Qy	241	LGCGSVITPLWIIAHCYDLYLPKSNTIQPGVSLDNPASHLVKEVIVESKYKPR	300						
Db	241	LGCGSVITPLWIIAHCYDLYLPKSNTIQPGVSLDNPASHLVKEVIVESKYKPR	300						
Qy	301	LGNDALMKLAGPLTENETQPYCLPNSNFPDGKVCTSGNATEDGDASPVNLNA	360						
Db	301	LGNDALMKLAGPLTENETQPYCLPNSNFPDGKVCTSGNATEDGDASPVNLNA	360						
Qy	361	VPLISNKICNRHDYGGIISPMSMLCAGYLTDGVDSCQGSPGVLVCQERRLWKLVGATSF	420						
Db	361	VPLISNKICNRHDYGGIISPMSMLCAGYLTDGVDSCQGSPGVLVCQERRLWKLVGATSF	420						
Qy	421	GIGCAEVNPKGYTRVTSFLDWIHEQMERDLKT	453						
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ID	ABU89858	standard; protein; 453 AA.							
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AC	ABU89858;								
XX									
DT	11-AUG-2003	(first entry)							
XX									
DE	Novel human secreted and transmembrane protein PRO382.								
XX									
KW	Human; Gene therapy; tissue typing; tumour; chondrocyte proliferation;								
KW	chondrocyte differentiation; tumour necrosis factor-alpha release;								
KW	affinity purification.								
XX									
OS	Homo sapiens.								
PN	US2003036147-A1.								
XX									
PD	20-FEB-2003.								
XX									
PF	02-JUL-2002;	2002US-00187741.							
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PR	18-SEP-1997;	97US-0059263P.							
PR	18-SEP-1997;	97US-0059466P.							
PR	17-OCT-1997;	97US-0062250P.							
PR	21-OCT-1997;	97US-0063486P.							
PR	24-OCT-1997;	97US-0063120P.							
PR	28-OCT-1997;	97US-0063121P.							
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PR	10-MAR-1998;	98US-0077450P.							
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PR	09-APR-1998;	98US-0081195P.							
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PR	22-APR-1998;	98US-0082704P.							
PR	28-APR-1998;	98US-0083122P.							
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PR	05-MAY-1998;	98US-0084146P.							
PR	06-MAY-1998;	98US-008414P.							
PR	07-MAY-1998;	98US-008440P.							
PR	07-MAY-1998;	98US-008443P.							
PR	15-MAY-1998;	98US-0085779P.							
PR	28-MAY-1998;	98US-008580P.							
PR	15-MAY-1998;	98US-008582P.							
PR	02-JUN-1998;	98US-0085700P.							
PR	02-JUN-1998;	98US-008759P.							
PR	03-JUN-1998;	98US-008727P.							
PR	04-JUN-1998;	98US-008825P.							
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PR	04-JUN-1998;	98US-008833P.							
PR	04-JUN-1998;	98US-0088326P.							
PR	05-JUN-1998;	98US-008832P.							
PR	05-JUN-1998;	98US-0088317P.							
PR	09-JUN-1998;	98US-008855P.							
PR	10-JUN-1998;	98US-008822P.							
PR	10-JUN-1998;	98US-008838P.							
PR	10-JUN-1998;	98US-008811P.							
PR	12-JUN-1998;	98US-008824P.							
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PR	17-JUN-1998;	98US-008838P.							
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 PR PR 24 - SEP-1998; 98US-0101743P.
 PR PR 24 - SEP-1998; 98US-0101742P.
 PR PR 25 - SEP-1998; 98US-0101786P.
 PR PR 29 - SEP-1998; 98US-010207P.
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 PR PR 01 - OCT-1998; 98US-0102644P.
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 PR PR 02 - OCT-1998; 98US-010295P.
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Query Match 100.0%; Score 2443; DB 6; Length 453;
 Best Local Similarity 100.0%; Pred. No. 3.8e-188;
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGENDPPDAVEAFSRSFLFGDDLKLKSPVAPADAAVAQIISULLPKFFPPIIVIGITALI 60
 Db 1 MGENDPPDAVEAFSRSFLFGDDLKLKSPVAPADAAQIISULLPKFFPPIIVIGITALI 60

Qy 61 LALAIGLGIHFDGSGKYRCRCSFKCIBELIARCDGVSDCKDGEDEYRCVRGQQNAVILQVF 120
 Db 61 LALAIGLGIHFDGSGKYRCRCSFKCIBELIARCDGVSDCKDGEDEYRCVRGQQNAVILQVF 120

Db 121 TAASWKTMCSDDWKGHTANVACAGLQPFSSYVSSDNLRVSSLEQGQFREEFVSIDHLPLDK 180
 Db 121 TAASWKTMCSDDWKGHTANVACAGLQPFSSYVSSDNLRVSSLEQGQFREEFVSIDHLPLDK 180

Qy 181 VDALHHVVYTRGGCAASGHVITLQCTAGHRRYSSRITVGGMSLISLQWPQMSLQFCQGYH 240
 Db 181 VPALHHSYYVREGCASHVVTLQCTAGHRRYSSRITVGGMSLISLQWPQMSLQFCQSYH 240

Qy 241 LGCGSVITPLWITTAACVYDLYLPKSWTIQVGLVSLIDNPAPSHLVKEVIVHSKYKPKR 300
 Db 241 LGCGSVITPLWITTAACVYDLYLPKSWTIQVGLVSLIDNPAPSHLVKEVIVHSKYKPKR 300

Qy 301 LGNDIAIMKLAGPLTENEMIQPVCPLNISEENFPDGKVYCWTSGMATEDGGDASPVLNHA 360
 Db 301 LGNDIAIMKLAGPLTENEMIQPVCPLNISEENFPDGKVYCWTSGMATEDGGDASPVLNHA 360

Qy 361 VPLISNKICNHHDVYGGTISPSMLCAGYLTCGVDSCQGDGGPLVLCQERRLWKLVGATSF 420
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RESULT 14
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 XX DT 09-JUL-2003 (first entry)
 DE Human; cancer related protein SEQ ID NO:206.
 KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KW heart disease; atherosclerosis; endometriosis.
 OS Homo sapiens.
 XX WO2003025138-A2.

PR 15-APR-1998; 98US-0081838P.
 PR 21-APR-1998; 98US-0082568P.
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 PR 21-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082797P.
 PR 28-APR-1998; 98US-0083322P.
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 PR 02-JUL-1998; 98US-0091632P.
 PR 02-JUL-1998; 98US-0094006P.
 PR 02-JUL-1998; 98US-0094008P.
 PR 04-AUG-1998; 98US-009582P.
 PR 10-AUG-1998; 98US-009598P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 18-AUG-1998; 98US-0096595P.
 PR 18-AUG-1998; 98US-009757P.
 PR 17-AUG-1998; 98US-009766P.
 PR 26-AUG-1998; 98US-0096676P.
 PR 17-AUG-1998; 98US-009691P.
 PR 17-AUG-1998; 98US-0096917P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 18-AUG-1998; 98US-0097022P.
 PR 26-AUG-1998; 98US-0097198P.
 PR 17-AUG-1998; 98US-009754P.
 PR 26-AUG-1998; 98US-0097955P.
 PR 26-AUG-1998; 98US-0098619P.
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 PR 26-AUG-1998; 98US-0098814P.
 PR 01-SEP-1998; 98US-009816P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0099502P.
 PR 10-SEP-1998; 98US-0099514P.
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 PR 01-SEP-1998; 98US-0098723P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 16-SEP-1998; 98US-0101751P.
 PR 16-SEP-1998; 98US-0101753P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100819P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101414P.
 PR 18-SEP-1998; 98US-010168P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101866P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0102070P.
 PR 29-SEP-1998; 98US-010240P.
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 PR 29-SEP-1998; 98US-010231P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-010251P.
 PR 01-OCT-1998; 98US-010254P.
 PR 01-OCT-1998; 98US-0102887P.

Query Match Similarity 100.0%; Score 2443; DB 6; Length 453;
 Best Local Similarity 100.0%; Pred. No. 3.8e-188;
 Matches 453; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

Qy 1 MGENDPPAVEAPPSFRSLIQLDKISPVAPDADAVAAQILSLLPLKFFPIIVIGITALI 60
 Db 1 MGENDPPAVEAPPSFRSLIQLDKISPVAPDADAVAAQILSLLPLKFFPIIVIGITALI 60
 Qy 61 LALATGLLGHFDGCKYRCSPECIELTARCDSQDKDGEDEYRCVGGONAVIQLF 120
 Db 61 LALATGLLGHFDGCKYRCSPECIELTARCDSQDKDGEDEYRCVGGONAVIQLF 120
 Qy 121 TAASKTMSDDWCHYANAVACAQIGFPSSVSSDNLRVSLEQFREBBFSIDHLLPDKX 180
 Db 121 TAASKTMSDDWCHYANAVACAQIGFPSSVSSDNLRVSLEQFREBBFSIDHLLPDKX 180
 Qy 181 VTALEHHSVTVREGCASHVTLQCTACGHRRGYSSRIVGNGMSLSSONPWOASLQFOQYH 240
 Db 181 VTALEHHSVTVREGCASHVTLQCTACGHRRGYSSRIVGNGMSLSSONPWOASLQFOQYH 240
 Qy 241 LGGSVITPLWIIAHCVTDLYLPKSWTQVGLSLLNPASHLVEKIVTHSKYKPKR 300
 Db 241 LGGSVITPLWIIAHCVTDLYLPKSWTQVGLSLLNPASHLVEKIVTHSKYKPKR 300
 Qy 301 LGNDIALMKLAGPLTFNEMIQFCVLPSBNFPGKVKUTSGWGATEDGDAASPVLNEA 360
 Db 301 LGNDALMKLAGPLTFNEMIQFCVLPSBNFPGKVKUTSGWGATEDGDAASPVLNEA 360
 Qy 361 VPLISNKICNRHDYGGIISPMLCAGYLGGDSCQGGPLVCQBERLWKLVGATSF 420
 Db 361 VPLISNKICNRHDYGGIISPMLCAGYLGGDSCQGGPLVCQBERLWKLVGATSF 420
 Qy 421 GIGCAEVNKGPGVYTRVTSFLDIHEQMERDJKT 453
 Db 421 GIGCAEVNKGPGVYTRVTSFLDIHEQMERDJKT 453

Search completed: May 5, 2004, 15:46:51
 Job time : 63 secs

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OM protein - protein search, using sw model.

Run on: May 5, 2004, 15:44:20 ; Search time 45 Seconds
 (without alignment)
 3176.217 Million cell updates/sec

Scoring table: BLOSUM62

Title: US-09-846-512-2

Perfect score: 24.3

Sequence: 1 MGENDDPAVEAPEFSRSLFG.....TRVTSFLDTHEQMERDLKT 453

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_rhbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_fodent:*
- 12: sp_virus:*
- 13: sp_vertebrata:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Database : SPTREMBL25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

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14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

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15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrata:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_fodent:*

DR	PRINTS;	P00722; CHYMOTRYPSIN.
SQ	SEQUENCE	PS00135; TRYPSIN SER; 1. SEQUENCE 453 AA; 49505_MW; 1E7EC6CB3DD894 CRC64;
Query Match	Score 91.1%; Best Local Similarity 89.0%; Matches 403; Conservative	Score 2225; DB 11; Length 453; Pred. No. 6.3e-207; Mismatches 25; Indels 0; Gaps 0;
Qy	1 MGENDPAAEPPFSRSLFGIDDLKISKPVAPDAVAQIQLLILKFPPIVIGIALLI 1 MGENDPAAEPPFSRSLFGIDDLKISKPVAPDGAVAAQIQLLILKFPPIVIGIALLI	1 MGENDPAAEPPFSRSLFGIDDLKISKPVAPDAVAQIQLSILKFPPIVIGIALLI 1 MGENDPAAEPPFSRSLFGIDDLKISKPVAPDGAVAAQIQLLILKFPPIVIGIALLI
Db	61 LALAIGGIGHDCSGYRCRSEKKCTELIARCD3SDCKDGEDEYRCVRYGGQAVIYF 61 LALAIGGIGHDCSGYRCRSEKKCTELIARCD3SDCKDGEDEYRCVRYGGQAVIYF	61 LALAIGGIGHDCSGYRCRSEKKCTELIARCD3SDCKDGEDEYRCVRYGGQAVIYF 61 LALAIGGIGHDCSGYRCRSEKKCTELIARCD3SDCKDGEDEYRCVRYGGQAVIYF
Qy	61 TAAWNKTMCSDDWKGHYANVACAQLEPPTSYSSDNLRVSSLEGDFREEFVSDHLLPDK 61 TAAWNKTMCSDDWKSHYANVACAQLEPPTSYSSDHLLPDK	61 TAAWNKTMCSDDWKGHYANVACAQLEPPTSYSSDNLRVSSLEGDFREEFVSDHLLPDK 61 TAAWNKTMCSDDWKSHYANVACAQLEPPTSYSSDHLLPDK
Db	121 TAAWNKTMCSDDWKSHYANVACAQLEPPTSYSSDNLRVSSLEGDFREEFVSDHLLPDK 121 TAAWNKTMCSDDWKSHYANVACAQLEPPTSYSSDHLLPDK	121 TAAWNKTMCSDDWKGHYANVACAQLEPPTSYSSDNLRVSSLEGDFREEFVSDHLLPDK 121 TAAWNKTMCSDDWKSHYANVACAQLEPPTSYSSDHLLPDK
Qy	181 VITALHHSVYREGCASHVVLQCTAGHRGGYSSRIVGGNMSLSQLPQASLOFGITH 181 VITALHHSVYREGCASHVVLQCTAGHRGGYSSRIVGGNMSLSQLPQASLOFGITH	181 VITALHHSVYREGCASHVVLQCTAGHRGGYSSRIVGGNMSLSQLPQASLOFGITH 181 VITALHHSVYREGCASHVVLQCTAGHRGGYSSRIVGGNMSLSQLPQASLOFGITH
Db	241 LGGSVITPLWTTAAHCVDYLPLKSWTQVGLVSLDNPAPSHLVEKTVHSCKPKR 241 LGGSVITPLWTTAAHCVDYLPLKSWTQVGLVSLDNPAPSHLVEKTVHSCKPKR	241 LGGSVITPLWTTAAHCVDYLPLKSWTQVGLVSLDNPAPSHLVEKTVHSCKPKR 241 LGGSVITPLWTTAAHCVDYLPLKSWTQVGLVSLDNPAPSHLVEKTVHSCKPKR
Qy	301 LGNDIAALKLAKPLFTNEIMIQPVCLPNSSEENFPDGKVWTSGWGAEDGGDASPVNHAA 301 LGNDIAALKLAKPLFTNEIMIQPVCLPNSSEENFPDGKVWTSGWGAEDGGDASPVNHAA	301 LGNDIAALKLAKPLFTNEIMIQPVCLPNSSEENFPDGKVWTSGWGAEDGGDASPVNHAA 301 LGNDIAALKLAKPLFTNEIMIQPVCLPNSSEENFPDGKVWTSGWGAEDGGDASPVNHAA
Db	361 VPLISNKICNRDVYGGIISPSPMLCAGYLTGGDSCOGDSGGPLVYQERBLWKLVGATSP 361 VPLISNKICNRDVYGGIISPSPMLCAGYLTGGDSCOGDSGGPLVYQERBLWKLVGATSP	361 VPLISNKICNRDVYGGIISPSPMLCAGYLTGGDSCOGDSGGPLVYQERBLWKLVGATSP 361 VPLISNKICNRDVYGGIISPSPMLCAGYLTGGDSCOGDSGGPLVYQERBLWKLVGATSP
Qy	421 GIGCAETVKPGYVTRTSFLDWTIQNEDLKLT 453 421 GIGCAETVKPGYVTRTSFLDWTIQNEDLKLT 453	421 GIGCAETVKPGYVTRTSFLDWTIQNEDLKLT 453 421 GIGCAETVKPGYVTRTSFLDWTIQNEDLKLT 453
Db	RESULT 2 Q8WY52 PRELIMINARY; PRT; 344 AA. ID Q8WY52 AC Q96T73 ID Q96T73 PRELIMINARY; PRT; 492 AA. ID Q8WY52 DT 01-MAR-2002 (TREMBLrel. 20, Created) ID DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update) ID DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update) ID DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	RESULT 3 ID Q8WY52 AC Q96T73 ID Q96T73 PRELIMINARY; PRT; 492 AA. ID Q8WY52 AC Q96T73 ID Q96T73 PRELIMINARY; PRT; 492 AA. ID Q8WY52 DT 01-DEC-2001 (TREMBLrel. 19, Created) ID DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) ID DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
OS	Homo sapiens (Human).	Homo sapiens (Human).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID	9606; [1]	9606; [1]
RN	SEQUENCE FROM N.A. Yang Y.C., Chen S.Y., Chang M.S., Cloning and characterization of TMRSS3, a new member of the serine protease family", Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. - - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. EMBL: AF267741; AF56664.1; - InterPro: IPR00903; Cys-Ser trypsin, Peptidase and peptidolysis; IEA. GO: GO:00016020; C:membrane, IEA. GO: GO:0004263; C:membrane, IEA. GO: GO:0008233; F:peptidase activity; IEA. GO: GO:0005044; F:scavenger receptor activity; IEA. GO: GO:0004295; F:trypsin activity; IEA. GO: GO:0006108; F:proteolysis and peptidolysis; IEA. InterPro: IPR00903; Cys-Ser trypsin, Peptidase and peptidolysis; IEA. InterPro: IPR02172; JBL receptor, IEA. InterPro: IPR01554; Peptidase S1-A. InterPro: IPR001314; Peptidase S1A. InterPro: IPR001190; Srrc receptor, IEA. PFam: PF00089; trypsin, IEA. InterPro: IPR03903; Cys-Ser trypsin, IEA.	SEQUENCE FROM N.A. Yang Y.C., Chen S.Y., Chang M.S., Cloning and characterization of TMRSS3, a new member of the serine protease family", Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. - - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. EMBL: AF267741; AF56664.1; - InterPro: IPR00903; Cys-Ser trypsin, Peptidase and peptidolysis; IEA. InterPro: IPR02172; JBL receptor, IEA. InterPro: IPR01554; Peptidase S1-A. InterPro: IPR001314; Peptidase S1A. InterPro: IPR001190; Srrc receptor, IEA. PFam: PF00089; trypsin, IEA. InterPro: IPR03903; Cys-Ser trypsin, IEA.

InterPro; IPR001254; Peptidase S1.	RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Boak S.A., McEwan P.J., McKernan K.J., Malek A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Gibbs R.A., Villafranca D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbons R.A., Fahay J., Heitton E., Kettman M., Madan A., Rodriguez G.J., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krywinski M.I., Skalska U., Smailus D.E., Schein J.E., Jones S.J., Marrs M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
InterPro; IPR001314; Peptidase S1A.	[2].
InterPro; IPR001190; Src receptor.	RN
PRINTS; PR0722; CHYMOTRYPSIN.	RA
SMART; SM00192; LDLA_1.	RA
SMART; SM00202; SRP_1.	RA
SMART; SM00220; TRYSP_SPC_1.	RA
PROSITE; PS01209; LDIFRA_1; 1.	RA
PROSITE; PS00668; LDIFRA_2; 1.	RA
PROSITE; PS0287; TRCR_2; 1.	RA
PROSITE; PS00240; TRPSIN_DOM; 1.	RA
PROSITE; PS00134; TRPSIN_HIS; 1.	RA
PROSITE; PS01335; TRPSIN_SER; 1.	RA
KW Hydrolase; Protease; Serine protease.	RN
SEQUENCE 492 AA; 53863 MW; 3ABA:55BF276DADF CRC64;	RN
Query Match 36.1%; Score 882; DB 4; Length 492; Best Local Similarity 45.7%; Pred. No. 1.3e-16; Matches 188; Conservative 54; Mismatches 149; Indels 20; Gaps 10;	RA
Qy 52 IVIGIAILALAILGLGIH--DCSGK-YRCRSSFXKCIELIARCDGVSDGKDEBEYRC 107	RA
Db 89 LTIGFLVGAALLAGLNUFKMFSKCSNSGICDSSGTCTINPSNWCGVSHPGGEENRC 148	RA
Qy 108 VRYGGONAVLQYFTA--ASWKTCMSDDWKGHYANVAGAQLGP--SYVSSDNLRVSSLEGQ 164	RA
Db 149 VRLYGNPNFLQWMISSQRKSWHPVQCDQDWNENYGRAACKDMGYRNNFYSSQGIVDDSGSTS 208	RA
Qy 165 FREEFVSDHLLPDKTVAHLHSVYREGCAGHVTIQLTAGCHRGYS--SRTVGGNM 222	RA
Db 209 FMKLNTSAGVN--DIIZKLYHS---DACSSKAVSLSRLACAGVNLNSRSQRSSRIVGGS 261	RA
Qy 223 SLLSQWQPAQSLOFGHFLGGSVITPLWIIITRAHCY-YDLYLPKWSITQVGLV-SLLD 279	RA
Db 262 ALGAWMPHQVSLSHVQNTVHGCGSITTEFWIPTAAHCYKEPLNNPMWHITAFLAGLIRQSFMP 321	RA
Qy 280 NPAPSHLYKEVYTHSKYTKPKRLNDIALMKLAGPLTNEMIQPVCLPNSBENPDSQGD 339	RA
Db 322 YGA-GYQEVKISHPNYDSTKTRNDIALMKQPLTNDLVRPVCLPNPQNMLOPEOLCW 380	RA
Qy 340 TSGNGATEGGDASPVLNHAAYPLISNCTICHERDVYGGIISPSMLCGYLTGVDSCQGD 399	RA
Db 381 TSGNGATEEKGTSEVINAVALLIEFTORNSRYVNDMLTPAMICAGFLQGNDVDSQGD 440	RA
Qy 400 SGGLPLVQCERRFLVKGATSGIGCAETYNKPGTYTRYTSFLDWTHEOMRD 450	RA
Db 441 SGGBLVTSNNINWLGDTSGSGCAKARYPGVYGNXFTDWIYQMRAD 491	RA
RESULT 4	RA
Q7TN04 ID Q7TN04 PRELIMINARY; PRT; 490 AA.	RA
AC Q7TN04; Mammalia; Rodentia; Chordata; Craniata; Vertebrata; Euteleostomi; Murinae; Mus.	RA
OX NCBI_TaxID=10090; RN	RA
SEQUENCE FROM N.A. STRAIN=129; TISSUE=Breast tumor; MEDLINE=22388257; PubMedId=12477932; RX	RA
DT 01-OCT-2003 (TREMBrel. 25, Created) DT 01-OCT-2003 (TREMBrel. 25, Last sequence update) DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)	RA
DE Tmprss2 protein.	RA
OS Mus musculus (Mouse).	RA
OC Buharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Chordata; Craniata; Vertebrata; Euteleostomi; Muridae; Murinae; Rattus.	RA
NCBI_TaxID=10116; RN	RA
SEQUENCE FROM N.A. RP	RA

OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC	Xenopodinae; Xenopus.
NCBI_TaxID	8355;
RN	
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20363741; PubMed=10903442;
RA	Yamaoka K.; Takabatake T.; Takeshima K.;
RT	"Isolation and characterization of three novel serine protease genes from Xenopus laevis";
RT	Gene 252:409-416 (2000).
RL	CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR	EMBL: AB038497; BAB08217.1; - .
DR	HSSP: P00166; 1CHG.
DR	MEROPS: S01_0.9; - .
DR	GO: 0004263; F-chymotrypsin activity; IEA.
DR	GO: 0008233; F-peptidase activity; IEA.
DR	GO: 0004259; F-trypsin activity; IEA.
DR	GO: 0006508; P-proteolysis and peptidolysis; IEA.
DR	IntePro; IPR009003; Cys-Ser_trypsin.
DR	IntePro; IPR002172; LDL_receptor_A.
DR	IntePro; IPR001254; Peptidase_S1.
DR	IntePro; IPR001314; Peptidase_S1A.
DR	Pfam: PF00057; Ldl_recept_a_4.
DR	Pfam: PF00089; trypsin_1.
DR	PRINTS: PR00722; CHYMOTRYPSIN.
DR	PRINTS: PR00261; LDLRECEPTOR.
DR	SMART: SM00192; Ldla; 8.
DR	SMART: SM00020; TRYP_SPC; 1.
DR	PROSITE: PS01019; LDLRA_1; 8.
DR	PROSITE: PS00068; LDLRA_2; 2.
DR	PROSITE: PS00240; TRYPSIN_DOM; 1.
DR	PROSITE: PS00134; TRYPSIN_HIS; 1.
DR	PROSITE: PS00135; TRYPSIN_SRR; 1.
KW	Hydrolyase; Protease; Serine protease.
SEQUENCE	767 AA; 8601 MW; B056438796DE96E CRC64;
SQ	
Query Match	34.2%
Best Local Similarity	45.1%
Matches 175;	Pred. No. 7.1e-72;
Conservative	Mismatches 131;
	Indels 36; Gap 1.
Qy	78 RCRSSPFKCIELIARCDGVSDCKQCBDEYRCVRRGGQNAYLQE--TAASWKMCSDDD
Db	394 RCGSSYTSVCLSSQWCDGVSPCPYSEDEMSCVSYLPADFQLQYSTSVAWLVCSDD
Qy	136 HYANVACAGLF--PSYVSSDNLR-----VSSLEGFREFRSVDHLLPDDKVT
Db	454 DFGFRACQDFCYNGGSYNYRDTLNSPYAPNGYFKLYSGYWRSKF-----YI
Qy	186 HSVVREGCASGHVYLQCTACG-HRGYGRSSRTVGGMNSLLSOPWQASLQFGYHH
Db	503 YSSY---CYSGNVVSLHLCSGVSNSLVSRIYGFTANLGWPQWVNQLQTGVV
Qy	245 SVITPLWITAAHCVYDLVLPKS-WTIVQGLVSLLDNP---APSILYEKIVTHSKV
Db	559 STISPRKWTIAHCGYSYSSASGRWRFPG---TLTKSYNNSYASAYFERTIVHPGJ
Qy	300 RLGNDAFLMKLAGPLTFENIMIQPVCLPNSEENFPDGKVWTSGWATEDDGDAASPVI
Db	616 TYNDALMKLDRTEFGTTOPVLPNSGMFWBAGTTWISGMGSTYEGGSVSTY

RESULT 6		RESULT 7	
Q9DGR2	PRELIMINARY;	Q7ZB80	PRELIMINARY;
Q9DGR2	PRT;	ID	PRT;
AC	767 AA.	AC	326 AA.
TT	(TREMBrel. 16, Created)	DT	
01-MAR-2001	(TREMBrel. 16, Last sequence update)	01-MAR-2001	(TREMBrel. 16, Last annotation update)
01-OCT-2003		01-OCT-2003	
DE	Embryonic serine protease-2	DE	XESP-2
XENOPUS LAEVIS	(African clawed frog).	XENOPUS LAEVIS	

AC Q72ZB0;	DT 01-JUN-2003 (TREMBLrel. 24, Created).	Db 297 YTSISBALTWIEQNE 312
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update).		
DE SI:z269G1_0.3 (Novel protein similar to human transmembrane protease, serine 3 (TMRSS3)) (Fragment).	RESULT 8	
GN SI:DZ69G1_0.3.	ID Q9BYE2, PRELIMINARY; PRT: 581 AA.	
OS Brachydanio rerio (Zebrafish) (Danio rerio).	AC Q9BYE2,	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.	DT 01-JUN-2001 (TREMBLrel. 17, Created)	
OC NCBI_TaxID=7955;	DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
OX [1]	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
RN RP SEQUENCE FROM N.A.	DE Membrane-type mosaic serine protease.	
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.	GN NCBI_TaxID=9606;	
EMBL; Alt72083; CA61105.1; -	OS Homo sapiens (Human).	
DR GO:0016021; C:integral to membrane; IEA.	OC Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo.	
DR GO:0004263; F:chymotrypsin activity; IEA.	RA Kido H.; Inoue M.; Kim D.R., Sharnain S.;	
DR GO:0008233; F:peptidase activity; IEA.	RA "Cloning and expression of novel mosaic serine proteases with and without a transmembrane domain from human lung.";	
DR GO:0005044; F:scavenger receptor activity; IEA.	RT Biochim. Biophys. Acta 1518:204-209 (2001).	
DR GO:0004295; F:trypsin activity; IEA.	RL EMBL; AB048796; BAB39741.1; -.	
DR GO:0006508; P:proteolysis and peptidolysis; IEA.	DR HSSP; P00753; IDPO.	
DR InterPro; IPR009003; Cys_Ser_trypsin.	DR MEROPS; S01_087; -.	
DR InterPro; IPR002172; LDL_receptor_A.	DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.	
DR InterPro; IPR001324; Peptidase_S1.	DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.	
DR InterPro; IPR001190; Srcr_receptor.	DR Sequence FROM N.A.	
Pfam; PF00089; trypsin_1.	DR TISSUE=Lung;	
DR PRINTS; PR00722; CHYMOTRYPSIN.	DR MEDLINE=21167393; PubMed=11267681;	
DR SMART; SM00192; LDLA; 1.	DR Kim D.R., Sharnain S.;	
DR SMART; SM000202; SR; 1.	RA "Cloning and expression of novel mosaic serine proteases with and without a transmembrane domain from human lung.";	
DR SMART; SM00020; TRYPSIN; SPC; 1.	RT Biochim. Biophys. Acta 1518:204-209 (2001).	
DR POSITIVE; PS01209; LDLRA_1; 1.	RL EMBL; AB048796; BAB39741.1; -.	
DR POSITIVE; PS50068; LDLRA_2; 1.	DR HSSP; P00753; IDPO.	
DR POSITIVE; PS50281; SRCR_2; 1.	DR MEROPS; S01_087; Idl1_recep_a; 1.	
DR POSITIVE; PS50240; TRYPSIN_DOM; 1.	DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.	
DR POSITIVE; PS00134; TRYPSIN_HIS; 1.	DR InterPro; IPR002172; LDL_receptor_A.	
DR POSITIVE; PS00135; TRYPSIN_SER; 1.	DR InterPro; IPR001314; Peptidase_S1.	
KW Transmembrane; Protease.	DR InterPro; IPR001190; Srcr_receptor.	
NON_TER 1 1	DR Pfam; PF00089; trypsin_1.	
SEQUENCE 326 AA; 35561 MW; 8DF12214393CDB2 CRC64;	DR PRINTS; PR00722; CHYMOTRYPSIN.	
Query Match 33.3%; Score 813; DB 13; Length 326;	DR SMART; SM00192; LDLA; 1.	
Best Local Similarity 42.6%; Pred. No. 3.8e-70;	DR PROSITE; PS00134; TRYPSIN HIS; 1.	
Matches 160; Conservative 47; Nismatches 101; Indels 68; Gaps 4;	DR PROSITE; PS00135; TRYPSIN_SER; 1.	
Query 73 CGKTYCRNSSPCIELIARCDGVSDKGDDEYCVRGQNAVQLQVFTAASWNTMCD 132	KW Hydrolase; Pro tease; Series_pro tease.	
Db 5 CSGKFPCVVSSVCISRNNAVGQVDCQDGEELNCVRSQSHSLVQFVRGLRVTVCSEG 64	SEQUENCE 581 AA; 62689 MW; 4DAE24D7D5BA4A CRC64;	
Query 133 WKGHYNVACAOGLGPSSYSSDNLRVSSLEGQFREEFVSD1HLLPDDKYTAHLHSVYRE 192	Query Match 29.7%; Score 726.5; DB 4; Length 591;	
Db 65 WDSQLSLTACRQLG-----79	Best Local Similarity 38.2%; Pred. No. 2e-61; Indels 29; Gaps 10; Matches 158; Conservative 66; Mismatches 161;	
Query 193 GCASGHGVVTQLQTAGCHRGYSSRIVGGMSLSSQWPWASLQFOGYHLCGGSVITPLW 252	Db 161 LPL-----1 C V L J A V Y L I F Q W Q H G T R C S D C K 213	
Db 80 -----SRATSSRIVGVNYSKSGQPVWSLAVHQYJUGGSITISESI 123	Qy 44 LPKEFPIVIGLIALTLAIGLGLPFDKCIETIARCDVSDFCK 99	
Query 253 ITAAHCYCDYLIPKSMWVQTLQGLVSLLDNPARSHLVEKITYHKYKPKRNNDI ALMKLG 312	Db 161 LPL-----1 C V L J A V Y L I F Q W Q H G T R C S D C K 213	
Db 124 LTAAHCVFGFAQPVLMVQYAGINLPLSKAEAHSTEKIIYTHANFRSKSYDZALIKTL 183	Qy 93 100 DGDEYRCVRLQVFTAAAS-WKTCMCSDDWKGHTANVACQOLGPSSYVSSDLNR 157	
Query 313 PLTFNEMIQPLVLPNSENFPDGKVICWTSGMATEDGGDASPVLNHAAPLISNKICHNR 372	Db 214 LKSDELCLCVRPWDKSILKIVSGSSQWLPCISSWINDSYSEKTCTQLGESAHTEVA 273	
Db 184 PLTFENDIAPICLPENYESFRNGOMLISGMGATVDSGETSLSLHVAQPLLSNEKECFI 243	Qy 158 VSSLGGQFREEFVSD1LPPDKRVTALEHSSVYREGCASGHVTVLQCTACGHRGGYSSRI 217	
Query 373 DVYGGTISPSMCAGYLGTGVDSCQDGGPVLVQERRLWLVGATSPGGCAEVNPKGV 432	Db 274 -----HRDANSSTSLIRN--S TIQESLH-RSHCPSSQRYISLOCSHCG-LRAMTGR 321	
Db 244 G-----LNNWNYCTEFLR-GVGTCCQSDGGPLACQ-GSAVTLVGTGSWDENGRKVNPKGI 296	Qy 218 VGGNMSSLLISOWPQASLQFOGYHLCGGSVITPLWITTAAHCYDL-YLPKSWTICQGLV 275	
Query 433 YTRVTSFLDWIEQME 48	Db 322 VGGALASPSKWWQVSHLHPGTHICGTLIDAQWVITAHHFVTRKEVILBGKVVAGTS 381	
Query 276 SJLDNPAPSHLYKEVIVHSKYKPKRNNDI ALMKLG-----1 C V L J A V Y L I F Q W Q H G T R C S D C K 335	Qy 382 NLHOLPERASTAE-ILINSNTDEEDDYDIALMRSLKPLTSIAHTPACLPMHGQFSLN 440	
Query 336 KVWTSGKGATEDGGD-ASPVLNHAAPLISNKICHNRDVYGGTISPSMLCAGYLGGVD 394	Qy	

Db	156 DIKLNRSQEFAQLS-ARPGSLV--EBAWQPSNTNCPSGRIVSLKCSECG-ARPLASRIVG 210	144 RWWQASMTLGRSRHTCCSVLAPYVWTAAHCMYSFRLSRLLSWVRHAGIVS--HSAVRQ 201
Qy	220 GNNMLLSWPWQASLTLQQGQHLOGGSVITPAMITIAHCYDLYLPK--SWTIQVGLVL 277	285 H--LVEKLIVVHSKYKPERLGNDIAMKLAPLTFNEMIQVCLPNSENFPDGKVWTS 341
Db	211 GQAVASGRPWQASVNLGSRHTTCGGSVLAPYVWTAAHCMYSFRLSRLLSWVRHAGLV 269	202 HQGMVVEKTPHFLYSSQNHDVVALQLRTPINFSDTVSACLPAKECHPQGSQCVWVS 261
Qy	278 LQNPASH--LVEKIVYH SKYKRPKRLGNNDIALMKGAPLTENEMIQVCLPNSENFPD 334	342 GWGATEDG-GDASPVHLAAYVPLIISNKICNRDVGGTISPSMLCAGYLGGVDSQGDS 400
Db	270 -HSAVRQHQGTMYEKIIPHFLYSSQAQNHDVVALQLRTPINPSDIVSACVPAKEQHFFQ 328	262 GKHGTDPSHTHSSDQLQDTMVPLSTLCNSCMYSGALTRMLCAGYLGRADQGDS 321
Qy	335 GRVCWTSGWGAETDG-GDASPVHLAAYVPLIISNKICNRDVGGTISPSMLCAGYLGGV 393	401 GGPLVLCQERRLWKLVGAATSGFGCAEVNKGCAEVTRTFSFLDWHOME 448
Db	329 GSOCMVWSQGHDDPSHTHSSDQLQDTMVPLSTLCNSCMYSGALTRMLCAGYLGDRA 388	322 GGPLVLCPSGDTWHLVGVWSWRGCAEEPNRGTYAKTAEFLDWHTDVTQ 369
Qy	394 DSCQGDSSGPLYCQERRLWKLVGAATSGFGCAEVNKGCAEVTRTFSFLDWHOME 448	RESULT 14
Db	389 DACQGDSSGPLYCQERRLWKLVGAATSGFGCAEVNKGCAEVTRTFSFLDWHOME 448	Q8CDR0 PRELIMINARY; PRT; 455 AA.
Q8CJ16	SEQUENCE FROM N.A. ID Q8CJ16 PRELIMINARY; PRT; 371 AA.	AC Q8CDR0; AC 08CDR0; DT 01-MAR-2003 (TREMBLrel. 23, Created); DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update); DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update); DE Transmembrane protease.
AC	Q8CJ16_001	GN Mus musculus (Mouse)
DT	01-MAR-2003 (TREMBLrel. 23, Created)	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Rodentia; Murinae; Mus.
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	OC NCBI_TaxID=10090;
DE	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	OX NCBI_TaxID=10090;
GN	AMP.	RN [1]
OS	Rattus norvegicus (Rat).	RP SEQUENCE FROM N.A.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	RC STRAIN=c57BL/6J; TISSUE=Testis; MEDLINE=22354683; PubMed=12466651;
OX	RN [1]	RX RA
RN	IPRO00903	RA the RIKEN Genome Exploration Research Group Phase I & II Team; RT Analysis of the mouse transcriptome based on functional annotation of the RIKEN transcriptome.
RP	SEQUENCE FROM N.A.	RT RT 60,770 full-length cDNAs.; RL Nature 40:563-573 (2002).;
RC	IPRO00903	DR GO; GO:0016020; C:membrane; IEA.
RC	IPRO00903	DR GO; GO:0004233; F:chymotrypsin activity; IEA.
RC	IPRO00903	DR GO; GO:0005044; F:scavenger receptor activity; IEA.
RC	IPRO00903	DR GO; GO:004295; F:trypsin activity; IEA.
RC	IPRO00903	DR GO; GO:006598; P:proteolysis and peptidolysis; IEA.
RC	IPRO00903	DR InterPro; IPRO00903; CYS_Ser trypsin.
RC	IPRO00903	DR InterPro; IPRO0114; Peptidase_S1.
RC	IPRO00903	DR InterPro; IPRO01190; Srcr_1 receptor.
RC	IPRO00903	DR PFAM; PF00089; trypsin_1.
PRINTS	IPRO0722; CHYMOTRYPSIN.	DR PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS	PR00722; CHYMOTRYPSIN.	DR SMART; SM00020; TRYSPC; 1.
DR	IPRO00903	DR PROSITE; PS00287; TRYSPC; 1.
DR	IPRO00903	DR PROSITE; PS00240; TRIPSIN DOM; 1.
DR	IPRO00903	DR PROSITE; PS00134; TRIPSIN HIS; 1.
DR	IPRO00903	DR PROSITE; PS00135; TRAPSIN SER; 1.
KW	Protease.	SQ SEQUENCE 455 AA.; BE22EB2E7503C74B CRC64;
SEQUENCE	371 AA; 40694 MW; 89A64081D9A1FB26 CRC64;	Query Match Score 693.5; DB 11; Length 455;
Query Match Best Local Similarity 28.7%; Score 700.5; DB 11; Length 371; Matches 138; Conservative 55; Mismatches 140; Indels 15; Gaps 8;	Best Local Similarity 39.7%; Pred. No. 3.7e-59; Matches 150; Conservative 63; Mismatches 173; Indels 29; Gaps 11;	
Qy 109 RVGGQNQAVIQLQVFTAA--SWKTMCSDDMKGHYANVACQQLGPSPSYSSDNDRVSSLLEGQFR 166	52 IVIGILIALILAIGG--LGTHFDGSKYRCRSSFKCIELARCDGVSDCKDGEDEYR-- 106	
Db 29 RINGDILLEVQYRARPWLLVCEGHNPAFLGMHITCOSLGYFLRLQHKAVNLSDKLNTS 88	Db 50 VILGVLGLAGAGIASWVLLVLYWPPAPSISGTLOPEEMTNCPGVS---REBELPS 105	
Qy 167 BEFVSIDHLLPDKVTALHHSVYVRECASHVVTIQLCTAAGHRRYYSSRVGGNMLS 226	Qy 107 ----CVRGGQNQAVIQLQVFTAA--SWKTMCSDDMKGHYANVACQQLGPSPSYSSDNDRVSSL 159	
Qy 89 QEFAQLS-ARPGSLV--EBAWQPSNTNCPSGRIVSLKCSECG-ARPLASRIVG 143	Db 106 LPKTVSPRINGEDLLOVQVRAFPDWWLVBCHGWSPALGMHICKSJLHRLTQHKAVNL 165	
Qy 227 QWDWQASLQQFQGYTHLCGSSVITPLWITAAHCYDLYLPK--SWTIQVGILVSLDNPAKS 284	Qy 160 SLEGQPREEPVSDHLLPDDKOTALHHSVYREGCAASHVVTIQLCTAAGHRRYYSSRVGG 219	
Db 166 DIKLNRSQEFAQLS-ARPGSLV--EBSWKPSANCPPGRIVSLKCSECG-ARPLASRIVG 220	Db 166 DIKLNRSQEFAQLS-ARPGSLV--EBSWKPSANCPPGRIVSLKCSECG-ARPLASRIVG 220	

DR PROSITE; PS00134; TRYPSIN HIS; 1.
 DR PROSITE; PS00135; TRYPSIN SER; 1.
 Db 221 GQAVASGRWNQASLQQGYHLLGGSVITPLWITAAHCVYDLYPK-SWTIQVGLYSL 277
 DR GO:001620; C:membrane; IEA.
 DR GO:0004263; F:chymotrypsin activity; IEA.
 DR GO:0005044; F:scavenger receptor activity; IEA.
 DR GO:0004295; F:trypsin activity; IEA.
 DR GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro:IPR000859; CUB.
 DR InterPro:IPR009003; Cys_Ser_trypsin.
 DR InterPro:IPR002172; LDL_receptor_A.
 DR InterPro:IPR000998; MAM_domain.
 DR InterPro:IPR001254; Peptidase_S1.
 DR InterPro:IPR001314; Peptidase_S1A.
 DR InterPro:IPR001190; Srcr_receptor.
 DR Pfam:PF00431; CUB; 2.
 DR Pfam:PF00629; MAM; 1.
 DR Pfam:PF00530; SRCR; 1.
 DR Pfam:PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHMOTRIPSIN.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00192; LDL; 1.
 DR SMART; SM00137; MAM; 1.
 DR SMART; SM00202; SR; 1.
 DR SMART; SM00020; TTFP_SPC; 1.
 DR PROSITE; PS01188; CUB; 1.
 DR PROSITE; PS01203; LDILA_1; 1.
 DR PROSITE; PS50038; LDILA_2; 1.
 DR PROSITE; PS0740; MAM_1; 1.
 DR PROSITE; PS50060; MAM_2; 1.
 DR PROSITE; PS50287; SRQR_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR NON_TER SEQUENCE 777 AA; 8731 MW; A1B2F4ECF06D3A8 CRC64;
 DR FT 1; Best Local Similarity 37.1%; Pred. No. 1.5e-54;
 DR Matches 151; Conservative 64; Mismatches 143; Indels 45; Gaps 16;
 DR SQ Query Match 26.9%; Score 657.5; DB 11; Length 777;
 DR Matches 151; Conservative 64; Mismatches 143; Indels 45; Gaps 16;
 DR SQ 67 LGIHFDS-SGKVRCRSSFKCTELIARCGVSDCKDGDEDEVRCYR---VGGQNAVLTQVFT 121
 DR 391 LGIPPEQDDEFQKG-NCTPLGNICDSYPHCRRGSDEASCVRLNGTRSNNGLVQFN1 449
 Db 339 GSOQWVSGWHTGHDPSHTHSSDTLQDTMPVPLSTYPLISNKICNHHDVGTISPMCLAGYLTCGV 393
 Db 122 AASWKTMCSDDWKGHYANVACAQGLPSTYSSDNIRVSDEGQFREEFYSIDHLLPDKV 181
 Db 450 HSIWHIACAEWNTTQISNEVCHLIGLS- ANSSNPISSTCG--GPFTRVNQ----- 497
 Qy 182 TALHHHSVYVREG-CASGHVYTLOCT--ACGHR--GYSRRIVGGMNSLISQFWQASL 234
 Db 498 -APNGSLLILTPSLQCCQDSLILLQCNHKSCGEKVTYTKQSPKIVGSDAOAGANFWVVVL 556
 Qy 235 QFQGYNH-----LOGGSVITPLWITTAAHCVYDLYL-PKSWTIQVGL-VSLLDNP-A 282
 Db 557 ---YHEDRSIDRLLGASLSSDWVVAHCVTERNLDTTRWAVLGLIMQSNTISPVQ 612
 Qy 283 PSHLVEKIVYHSSKYKPKRLGNDIALMKLAPLTTENEMIQPVCLPNSEBNPPDGKVWTS 342
 Db 613 VRRVVDQIVINPHYDERRKNDIAMMHLFPRVNTIPIGRTSIAG 672
 Qy 343 WGATEDGGDASPVLNEHAAPLISNKTCONHR-DVYGGIIIPSMLCGQLTGVDSCQGDSG 401
 Db 673 WGYDKLNGSTVDYKEADVPLISNERCQOLPEYN-ITESMICAGYEEGSDSCQGDSG 730
 Qy 402 GPALVCQERRLWKLVAGTSFGIGCAVNPKGVYTRYVTSFLDWIH 444
 Db 731 GRIMCQENNMRNFVGTTSFGVOCALNHPGVYVRSQFIEWH 773

Search completed: May 5, 2004, 15:48:19
 Job time : 47 secs

RESULT 15
 Q8CAN9 PRELIMINARY; PRT; 777 AA.
 AC Q8CAN9_ (REMBrel. 23, Created)
 DT 01-MAR-2003 (REMBrel. 23, Last sequence update)
 DT 01-OCT-2003 (REMBrel. 25, Last annotation update)
 DE Proteas (Fragment).
 PRSS7 OR A13009/D2RIK.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] _
 RN Taxid=10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=C57BL/6J; TISSUE=Thymus;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL EMBL; AK038356; BAC29973.1;
 DR MGD: MGJ:1197523; PRSS7
 DR GO:001620; C:membrane; IEA.
 DR GO:0004263; F:chymotrypsin activity; IEA.
 DR GO:0005044; F:scavenger receptor activity; IEA.
 DR GO:0004295; F:trypsin activity; IEA.
 DR GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro:IPR000859; CUB.
 DR InterPro:IPR009003; Cys_Ser_trypsin.
 DR InterPro:IPR002172; LDL_receptor_A.
 DR InterPro:IPR000998; MAM_domain.
 DR InterPro:IPR001254; Peptidase_S1.
 DR InterPro:IPR001314; Peptidase_S1A.
 DR InterPro:IPR001190; Srcr_receptor.
 DR Pfam:PF00431; CUB; 2.
 DR Pfam:PF00629; MAM; 1.
 DR Pfam:PF00530; SRCR; 1.
 DR Pfam:PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHMOTRIPSIN.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00192; LDL; 1.
 DR SMART; SM00137; MAM; 1.
 DR SMART; SM00202; SR; 1.
 DR SMART; SM00020; TTFP_SPC; 1.
 DR PROSITE; PS01188; CUB; 1.
 DR PROSITE; PS01203; LDILA_1; 1.
 DR PROSITE; PS50038; LDILA_2; 1.
 DR PROSITE; PS0740; MAM_1; 1.
 DR PROSITE; PS50060; MAM_2; 1.
 DR PROSITE; PS50287; SRQR_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.

[...] number of hits containing chosen parameters.

maximum DB segment length: 2000000000

best - processing: Minimum Match 0%

Maximum Match 100%

הברון דבָּרְךָ אֶלְעָזָר

Database : Issued_Patents_AA:*

2: /cgn2_6/ptodata/2/iaa/5B

COMBINE: DECOMPOSITION

5: //cgn2--6--Ptoodata//2/iaa/PICTUS--COMB--PEP:*

6: /e/gn2_6/prodata/z/ida/backfilesi.pep1:

ed. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB ID			Description
		Match	Length	DB	
1	2385.5	97.6	454	3	US-09-518-046-2
2	2306	90.3	455	3	US-09-261-416-2
3	1354	55.4	294	3	US-09-511-046-4
4	885	36.2	492	3	US-09-312-749-2
5	885	36.2	492	4	US-09-691-840-2
6	874	35.8	492	4	US-09-685-1674-895
7	862	35.3	157	3	US-09-518-046-23
8	696	28.5	283	3	US-08-807-151-1
9	696	28.5	283	4	US-09-477-1
10	674	27.6	417	4	US-09-820-002-4
11	669.5	27.4	798	1	US-08-200-900A-2
12	669.5	27.4	798	5	PCT-US94-00616-2
13	665.5	27.2	423	4	US-09-656-002-4
14	665	27.2	416	2	US-09-000-946-2
15	658	26.9	435	3	US-09-008-271LA-6
16	658	26.9	437	4	US-09-851-588-8
17	656.5	26.9	376	4	US-09-820-002-2
18	656.5	26.9	406	4	US-09-851-588-6
19	585.5	24.0	256	2	US-09-027-337-3
20	585.5	24.0	256	4	US-09-644-600-3
21	585.5	24.0	256	4	US-09-644-480-3
22	580.5	23.8	255	3	US-08-944-483-67
23	579.5	23.7	638	2	US-08-681-151-3
24	571	23.4	418	1	US-08-508-448C-25
25	571	23.4	418	4	US-09-370-838-82
26	571	23.4	418	4	US-09-370-838-83
27	571	23.4	418	4	US-09-370-838-83

FAILURE: OTHER INFORMATION: complete amino acid sequence of TADG-112

OTHER INFORMATION: Protein						
	US-09-518-046-2	Query Match	Best Local Similarity	Score	Length	
Matches	444;	Conservative	97.6%	2385.5;	DB 3;	Length 454;
Qy	1	MGENDDPPEAEPFSRLFGQLDLKISPVAPDADAYAQIQLLSPKFF-PILIVGIGLIAL	97.8%	Pred. No. 1.3e-223;	Index 7;	Gaps 1;
Db	1	MGENDDPPEAEPFSRLFGQLDLKISPVAPDADAYAQIQLLSPKFF-PILIVGIGLIAL	97.8%	2;	Missmatches 7;	
Qy	60	ILALAGIGHFPHCSCGKYRCRSSFKCTELIARCQGDCKDGDEYRVCVRGGQNAYLQV	97.5%	119		
Db	61	ILALAGIGHFPHCSCGKYRCRSSFKCTELIARCQGDCKDGDEYRVCVRGGQNAYLQV	97.5%	119		
Qy	120	FTAAWKTMCSDWKGHYANVACAQLGFPSPYSSDNLRVSSLEGFQFEEFYSIDHLLPDD	97.5%	179		
Db	121	FTAAWKTMCSDWKGHYANVACAQLGFPSPYSSDNLRVSSLEGFQFEEFYSIDHLLPDD	97.5%	179		
Qy	180	KYTALHHSVYREGGASHVVTIQLCTAGHRRGYSRSVVGGMNSLISOWPWAQSLQFGY	97.5%	239		
Db	181	KYTALHHSVYREGGASHVVTIQLCTAGHRRGYSRSVVGGMNSLISOWPWAQSLQFGY	97.5%	239		
Qy	240	HLCGGSVITPLWITAHHCVYDLYLPKSWTIQLQGLVSLLDNPAWPASHLVEKIVTHSKYKPK	97.5%	299		
Db	241	HLCGGSVITPLWITAHHCVYDLYLPKSWTIQLQGLVSLLDNPAWPASHLVEKIVTHSKYKPK	97.5%	299		
Qy	300	RLGNDAIMKLKAGPLTFNPMIQPVCLPSEENFPDGKVTCWTSMGKATEDGGDASPVLNHA	97.5%	359		

RESULT 2

US-09-261-416-2

Sequence 2, Application US/09261416A

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

PATENT NO.: 6291663

FILE REFERENCE: D619CIP

TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed in Ovarian Carcinoma and Uses Thereof

CURRENT APPLICATION NUMBER: US/09/518-046

CURRENT FILING DATE: 2000-03-02

EARLIER APPLICATION NUMBER: US/09/261-416

EARLIER FILING DATE: 1993-03-03

NUMBER OF SEQ ID NOS: 153

SEQ ID NO: 4

LENGTH: 294

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: complete amino acid sequence of TADG-12

OTHER INFORMATION: variant protein

US-09-518-046-4

Query Match Score 1354; DB 3; Length 294;

Best Local Similarity 88.1%; Pred. No. 1.6e-12;

Matches 255; Conservative 7; Mismatches 20; Indels 8; Gaps 2;

QY 1 MGENDPPAYEAPFSRSLFGDDDKISPVADDAVAQISSLPLKFF-PIVIGITAL 59

Db 1 MGENDPPAYEAPFSRSLFGDDDKISPVADDAVAQISSLPLKFF-PIVIGITAL 60

QY 60 ILALAIAGLIGHFDSGGKTCRCSSEFKCIEILARDGVSIICKDGEYRCVRYCGQNAVLQV 119

Db 61 ILALAIAGLIGHFDSGGKTCRCSSEFKCIEILARDGVSIICKDGEYRCVRYCGQNAVLQV 120

QY 120 FTASWKTMCSDDKKGHAYANVACQLGPSYVSSDNLRVSSLEQFQREFEFVSDHLLPDD 179

Db 121 FTASWKTMCSDDKKGHAYANVACQLGPSYVSSDNLRVSSLEQFQREFEFVSDHLLPDD 180

QY 180 KVTALHHSVYREGASGHVTVLQCTACHRGGYSSRVGGMSLSPWQASLQOLOGY 239

Db 181 KVTALHHSVYREGASGHVTVLQCTACHRGGYSSRVGGMSLSPWQASLQOLOGY 240

QY 240 HLCGESSVITPLWITAAHVCDYDLYLPKAWTIVGLVLV-----LNPAPSH 285

Db 241 HLCGESSVITPLWITAAHVCDYDLYLPKAWTIVGLVLV-----LNPAPSH 293

RESULT 4

US-09-342-749-2

Sequence 2, Application US/09342749

PATENT NO.: 6166194

GENERAL INFORMATION:

APPLICANT: Wong, Alexander K.C.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian Genetics, Inc.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor

FILE REFERENCE: 2318-202

CURRENT APPLICATION NUMBER: US/09/342-749

EARLIER APPLICATION NUMBER: US/09/342-749

EARLIER FILING DATE: 1999-06-29

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 2

LENGTH: 492

TYPE: PRT

ORGANISM: Homo sapiens

US-09-342-749-2

Query Match Score 885; DB 3; Length 492;

Best Local Similarity 46.0%; Pred. No. 1.4e-7;

Matches 189; Conservative 53; Mismatches 149; Indels 20; Gaps 10;

QY 360 AVPLISNKTCNRHDYGGG1ISPMSMCAGYLPGVWTGCGATGDDGASPVLNHA 359

Db 361 AVPLISNKTCNRHDYGGG1ISPMSMCAGYLPGVWTGCGATGDDGASPVLNHA 360

QY 415 VGATSEFGIGCAEVNPKPGVYTRVTSFLDWTHEQMERDLKT 453

Db 417 VGATSEFGIGCAEVNPKPGVYTRVTSFLDWTHEQMERDLKT 455

RESULT 3

US-09-518-046-4

Qy 52 IVIGIALLAIALIGLIGHF---DCSGK-YRCRSSFKCIELIARCDGYSDCDKGEDEYRC 107
 :
 Db 89 LTLGTFVLGAALAGLWMKFMGSXCSNSGIECDSSGTCPNSWCDGYSHCPGEDENRC 148

Qy 108 VRVGQNALQVYETA--ASWKTMCSDDWKGHRYANVACQALGFP-SYVSSDNLRYSSLEGQ 164
 :
 Db 149 VRLYGPNFLQVYSSQRKSWHPVQODDNENYGRAACRDGMYKANFYSSGRIVDGSQS 208

Qy 165 FREEFSIDHLPPDKVTAHHSTSYVREGCASGHVTIQCCTAGHRRGYS--SRIVGGMN 222
 :
 Db 209 FMKLNITSAGNV--DIYKLHYHS---DCISSRAVSVLRCIAVGVNINSRSRIVGES 261

Qy 223 SLLSQWPWQASLQFOQYHLCGGSVITPLWITTAHCV-YDLYLPKSNTIQVGLV--SLID 279
 :
 Db 262 ALPGAWPQVSLHVQVHVGGSITPEVITVAHCVPBLNPWHATAFGLRQSMF 321

Db 262 ALPGAWPQVSLHVQVHVGGSITPEVITVAHCVPBLNPWHATAFGLRQSMF 321

RESULT 6
 US-09-685-166A-895
 / Sequence 895, Application US/09685166A

Qy 280 NPAPHLVKEVIVTISKYKPRLGNDIAMKLAGLTENMIQPYCLPNSEENPDGYCW 339
 :
 Db 322 YGA-GYQVERVISHNYDSKTNNDIAMKLOQPLTENLVKPYCLPNPGMMLQPEOL-CW 380

Qy 340 TSGWGATEDGGSPLNHAAPLTSNKICNHRDVYGGJISPSMLCAGYLTCGyDSCQD 399
 :
 Db 381 ISGRGATEERGKTSSEVNAKULLETQRNSRVTYDNTITPAMICAEGQNVDSQGD 440

Qy 400 SGGPLVYCOERRLWKLUGATSFQGIGCAEVNPKGYTRTSFLDTHEQMRD 450
 :
 Db 441 SGGPLVTSKNIIWLLGDTSWSGCAKAYRPVIGNVMFTDWIYRQMRAD 491

RESULT 5
 US-09-691-840-2
 / Sequence 2, Application US/09691840
 / Patent No. 6444419

/ GENERAL INFORMATION:
 / APPLICANT: Wong, Alexander K.C.
 / APPLICANT: Tavtigian, Sean V.
 / APPLICANT: Teng, David H.-F.
 / APPLICANT: Myriad Genetics, Inc.

/ TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
 / CURRENT APPLICATION NUMBER: US/09/691,840
 / CURRENT FILING DATE: 2000-10-18
 / PRIOR APPLICATION NUMBER: US/09/342,749
 / PRIOR FILING DATE: 1999-06-29
 / PRIOR APPLICATION NUMBER: US 60/091,044
 / PRIOR FILING DATE: 1998-06-29
 / NUMBER OF SEQ ID NOS: 33
 / SEQ ID NO: 2
 / LENGTH: 492
 / TYPE: PRT
 / ORGANISM: Homo sapiens

Query Match 36.2%; Score 885; DB 4; Length 492;
 Best Local Similarity 46.0%; Pred. No. 1.4e-77;
 Matches 189; Conservative 53; Mismatches 149; Indels 20; Gaps 10;
 Organism: Homo sapiens

US-09-691-840-2

Query Match 35.8%; Score 874; DB 4; Length 492;
 Best Local Similarity 45.5%; Pred. No. 1.7e-76;
 Matches 186; Conservative 55; Mismatches 148; Indels 20; Gaps 10;

Qy 52 IVIGIALLAIALIGLIGHF---DCSGK-YRCRSSFKCIBELIARCDGVSDCKDGEDEYRC 107
 :
 Db 89 LTLGTFVLGAALAGLWMKFMGSXCSNSGIECDSSGTCPNSWCDGYSHCPGEDENRC 148

Qy 108 VRVGQNALQVYETA--ASWKTMCSDDWKGHRYANVACQALGFP-SYVSSDNLRYSSLEGQ 164
 :
 Db 149 VRLYGPNFLQVYSSQRKSWHPVQODDNENYGRAACRDGMYKANFYSSGRIVDGSQS 208

Qy 165 FREEFSIDHLPPDKVTAHHSTSYVREGCASGHVTIQCCTAGHRRGYS--SRIVGGMN 222
 :
 Db 209 FMKLNITSAGNV--DIYKLHYHS---DCISSRAVSVLRCIAVGVNINSRSRIVGES 261

Qy 223 SLLSQWPWQASLQFOQYHLCGGSVITPLWITTAHCV-YDLYLPKSNTIQVGLV--SLID 279
 :
 Db 262 ALPGAWPQVSLHVQVHVGGSITPEVITVAHCVPBLNPWHATAFGLRQSMF 321

Qy 280 NPAPHLVKEVIVTISKYKPRLGNDIAMKLAGLTENMIQPYCLPNSEENPDGYCW 339
 :
 Db 322 YGA-GYQVQKVISSHNYDSKTNNDIAMKLOQPLTENLVKPYCLPNPGMMLQPEOL-CW 380

RESULT 7
 US-09-518-046-23
 ; Sequence 23, Application US/09518046
 ; Patent No. 6294663
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; ADDRESS: 1000 University Ave, Seattle, WA 98101
 ; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
 ; in Ovarian Carcinoma and Uses Thereof
 ; FILE REFERENCE: D6112CIP
 ; CURRENT APPLICATION NUMBER: US/09/518,046
 ; CURRENT FILING DATE: 2000-03-02
 ; EARLIER APPLICATION NUMBER: 09/261,416
 ; EARLIER FILING DATE: 1999-03-03
 ; NUMBER OF SEQ ID NOS: 153
 ; SEQ ID NO 23
 ; LENGTH: 157
 ; TYPE: PRTE
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: protease domain of TADG-12 (TADG12)
 ; NAME/KEY: DOMAIN
 ; FEATURE:
 ; Query Match 35.3%; Score 862; DB 3; Length 157;
 ; Best Local Similarity 100.0%; Pred. No. 4; Ge-76; Length 157;
 ; Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; US-09-518-046-23

Query Match 35.3%; Score 862; DB 3; Length 157;
 ; Best Local Similarity 100.0%; Pred. No. 4; Ge-76; Length 157;
 ; Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; US-09-518-046-23

Qy 250 LWITAAHCVYDLYPLKSNTIQVLSLIDNPAPSHLYVEKIVHSKYKPKRGLNDIALMK 309
 Db 1 LWITAAHCVYDLYPLKSNTIQVLSLIDNPAPSHLYVEKIVHSKYKPKRGLNDIALMK 60

Qy 310 LAGPTENEMIQPVCLPNESEENFDGKV/CWTSGWATGGDASPVLNHAAPLISNKC 369
 Db 61 LAGPTENEMIQPVCLPNESEENFDGKV/CWTSGWATGGDASPVLNHAAPLISNKC 120

Qy 370 NHRDYGGTTSPSMICAGYLTDGYDSCQDGGPLVC 406
 Db 121 NHRDYGGTTSPSMICAGYLTDGYDSCQDGGPLVC 157

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/807,151
 ; FILING DATE: Filed Herewith
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: FF-0227 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-85-4166
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 283 amino acids
 ; TYPE: amino acid
 ; SPANNEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: SCORNTO01
 ; CLONE: 556016
 ; US-09-807-151-1

Query Match 28.5%; Score 696; DB 3; Length 283;
 ; Best Local Similarity 50.4%; Pred. No. 1,5e-59;
 ; Matches 137; Conservative 37; Mismatches 92; Indels 6; Gaps 4;

Qy 184 LHHSYVRECGASGSVVIQCIAGHRRQYS-SRIVGOMMSLISQNMQASIQFGYHL 241
 Db 12 TYKLYHSDACSSXAVSLRCIAGVNNSRSQRSVIGEASALPAMWQVSILHVQVNHV 71

Qy 242 CGGSVITTPMIIITAHHCV-YDLMLPKSWTIQVGLV--SLLDNPAHSLVKEVIVYHCKYP 298
 Db 72 CGGSVITTPMIIITAHHCV-EKPNPWHHTAFAGLLRQEFMPYGA-GCQYEKVISHPYNDS 130

Qy 299 KRLGNNDIAMLKLAGFLPTENEMIQPVCLPNESEENFDGKV/CWTSGWATGGDASPVLNH 358
 Db 131 KTRNDNDIAMLKQLQPLTENDLVKPCVLNPFGMNLQPEQLCWLISGWGATEEKGKTSEVINA 190

Qy 359 AAEPJLSNKICNHDYGGTIPSMLCAGYLTDGYDSCQDGGPLVCYDQVNLKLYSAT 418
 Db 191 ARVLLETQCNRSVYDNLITPAMICAFQLGNVDSCDGGXLVTSKNINWLLGDT 250

Qy 419 SFGIGGAEVNKGPGIYTRTSFEDWTHEQWED 450
 Db 251 SWGSGAKAYRPQYGVNVFTDWYRQRAD 282

RESULT 9

US-09-478-957-1
 ; Sequence 1, Application US/09478957
 ; Patent No. 6350448
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; ADDRESS: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/478, 957
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/807, 151
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36, 749
 REFERENCE/DOCKET NUMBER: PF-0227 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-0555
 TELEFAX: 415-845-1166
 SEQUENCE CHARACTERISTICS:
 LENGTH: 283 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: SCORNTO1
 CLONE: 556016

US-09-478-957-1

Query Match 1: Best Local Similarity 35.8%; Pred. No. 3.8e-57; Matches 149; Conservative 62; Mismatches 143; Indels 62; Gaps 11;

Qy 59 LILALAGILGIHDCSGKYRCRSSFKCIELIARCDGWSDCXDGEDBYRCYRGQONAVLQ 118
 Db 26 LILITAG-----AASWAVALIRSD-----QBPIPVQSSADRLM 64

Qy 119 VF-TAASWIKMCSDDWKHYANVACQQLGPPSYVSSDNLYVSSLEGQRSEPFVSDHLL 176
 Db 65 VFDKTEGIVWLICSSRSNARVGLSCBEMGFRLALTHSELUDVTRAGNTSGFFCVD-----122

Qy 177 PDDKVTALIHSVYRE---GCASGVVTLQCTACCHRGYSSRIVGAMSLLSQMPWQ 231
 Db 123 -----GRIPHTQBLLEVTPSPDPCRGRFLAAICQDGCCRKLPUVDRIVGGRTSLGRWPWQ 177

Qy 232 ASLQFOGYHLCGGSVITPLWITTAACHVYDLYPK-----SWTIQVGLVSLLDNAPSH 285
 Db 178 VSLRYGKAVYTHGGGLPFDPNSBENSIDALVHLSSSLPLTYIQPCPLPANGQALVDGK 289

Qy 286 L---VEKTVYHSKYKPKR-----LGNDIAALKLAGPLTFNEMIOPYCLPNSEENFDGK 336
 Db 230 LQLQVQAVYTHGGGLPFDPNSBENSIDALVHLSSSLPLTYIQPCPLPANGQALVDGK 289

Qy 337 VCWTSGWGATEDGGDASPVINHRAVPLISNKYCNHRDVYGGITSPSMICAGLTGCGDSC 396
 Db 290 ICYTIVGKGNTQOYQGOAQGLQEARVPITSNDVNGAFYGNOLKPKFECAGPEGGIDAC 349

Qy ; Sequence 2, Application US/08200900A
 Db ; Patent No. 5665566

Qy ; GENERAL INFORMATION:
 Db ; APPLICANT:
 Qy ; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
 Db ; NUMBER OF SEQUENCES: 38
 Qy ; CORRESPONDENCE ADDRESS:
 Db ; ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
 Db ; STREET: 87 Cambridge Park Drive
 Db ; CITY: Cambridge
 Db ; STATE: MA
 Db ; COUNTRY: USA
 Db ; ZIP: 02140

RESULT 11:

Qy 28.5%; Score 696; DB 4; Length 283;
 Best Local Similarity 50.4%; Pred. No. 1.6e-59;
 Matches 137; Conservative 37; Mismatches 92; Indels 6; Gaps 4;

Qy 184 LHHSVVYREGCAASGHVYTLQCTAGCHRRGYS--SRTIVGAMMSLLSQWPWQASLQFGYH 241
 Db 12 IYCKLYHSPACSSKAWSLRLCAGVNINNSQSRTIVGGESALPGAWPQSLRVNVHV 71

Qy 242 CGGSVITPWIIITAHCY YDLVLPKSWTIQGV- SLIDNPAPSHLVKEIYHSKYKP 298
 Db 72 CGGSVITPWIIITAHCYKEPKLNPNWHTAFAGLRQSFMPYGA-GYQVERVISHENYD 130

Qy 299 KRLNDIAALKLAGPLTPEMIPDVKCIPNSEEFPDKGVCTWSGKATEDGDASPVINH 358
 Db 131 KTKNDIAALKQKLPLTENDLVRPKVCLPNPGNMLOPESQCNLTSGWGATEKGKTSEVNA 190

Qy 359 AAYPLISNPKICHERDVGIIPSMLCAGYLTGVDSCQGDSCGPLYVCQERLWKVGA 418
 Db 191 ARVYLIEETQRCSRPYVYDNLITPAICFGLQNVDFQSGSGXVYTSKONIWWLIGDT 250

Qy 419 SFGIGCAENKPGVYTRYVFLWHEONERD 450
 Db 251 SWGSGCAKARYRPGVYGNVNFDTMITYROMRAD 282

Qy ; COMPUTER READABLE FORM:
 Db ; MEDIUM TYPE: Floppy disk
 Db ; COMPUTER: IBM PC compatible
 Db ; OPERATING SYSTEM: PC-DOS/MS-DOS
 Db ; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

RESULT 10:

US-09-820-002-4

Qy Sequence 4, Application US/09820002
 Db Patent No. 682630

Qy GENERAL INFORMATION:
 Db APPLICANT: Gan, Weiniu
 Db APPLICANT: Ye, Jane
 Db APPLICANT: DiFrancesco, Valentina
 Db APPLICANT: Beasley, Ellen

Qy TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
 Db TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
 Db TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CLO01194
 CURRENT APPLICATION NUMBER: US/09/820,002
 CURRENT FILING DATE: 2001-03-29
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4

Qy LENGTH: 417
 Db TYPE: PRT
 Db ORGANISM: HUMAN

Query Match 2: Best Local Similarity 27.6%; Score 674; DB 4; Length 417;

Query Match 3: Best Local Similarity 27.4%; Score 669.5; DB 1; Length 798;

Best Local Similarity 37.0%; Pred. No. 2.6e-56; Matches 146; Conservative 70; Mismatches 146; Indels 33; Gaps 14;

Qy 66 GLGHFDC-SGKTRCRSSRCIBIARCDGVSDCKDGEYRCVRV-- -GGNAVILQVF 120
 Db 415 GLGIPERCPEDNPKQKD-G-ECIPLVNLCDGPCKDSDAEAVRLNGTDSGLYQFR 473
 Qy 121 TAASWKTMCSDDKGHYANVACAGLGPSPYVSSDNLRVSLECGQFREBVSIDHLLPDDK 180
 Db 474 IQSIVMVAEENWTQISDVQCLGLGT-- -GNNSVPTFSTG-- -GPVNIN----- 521
 Qy 181 VTAHHHSVYY--REGCASHVVTLOCT--ACGHR--RGYSSRIVGNNMSLUSQWPAOS 233
 Db 522 -TAPNGSLILTPSQQCLESLILQCNYSCKKLTVQVSPKIVGSDREGAWPVVA 580
 Qy 234 LQFGSYHUGGSVITPLNLTAAHCYDYL-PKSWTIQVGL--VSLIDNP-APSHIVEK 289
 Db 581 LYFDDQYQCAISLYSRDWNVAASAHCVGNMBSKWKAVLGMAASNTSPQETRIDQ 640
 Qy 290 IVYHSKYKPKRGNIDLAMKLAGBLTENEMIOPVCLPNEISEENFPDGKVCMWSGWGATEDG 349
 Db 641 IVINPHYNKRKNDIAMMHLKMYNTYIOPICLPEENQVPPGRCISIAGWGALIYQ 700
 Qy 350 GDASPVLNHAAPVLINSNKICNHR-DVYGGIISPMSMLCAGYLTTGVDSCQGDGGPLVCQE 408
 Db 701 GSTADVLQADPVLSNECQQMPENY-ITENMVCAEGVDSQGDGGPLMCQE 758
 Qy 409 RRLWKLVGATSGFGCAENKPGVYTRYTSFLDWI 443
 Db 759 NNRWLLAGVTSFGTQCALNRPGYARYPRFTEWI 793

RESULT 13
 US-09-656-002-2
 Sequence 2, Application US/09656002
 ; Patent No. 6455668
 ; GENERAL INFORMATION:
 ; APPLICANT: Mack, David
 ; ATTORNEY: Gish, Kurt
 ; INVENTOR: Willcox, Keith
 ; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSTING COLORECTAL CANCER, COMPOSITIONS, AND A FILE REFERENCE: A-691-08/DIB/JUD/AMS
 ; CURRENT APPLICATION NUMBER: US/09/656,002
 ; PRIOR APPLICATION NUMBER: US/09/525,993
 ; CURRENT FILING DATE: 2000-09-06
 ; PRIOR FILING DATE: 2000-03-15
 ; PRIOR APPLICATION NUMBER: US 09/493,444
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: PCT/US 00/07044
 ; SEQ ID NO: 3
 ; NUMBER OF SEQ ID: NOS: 3
 ; SOFTWARE: PatentIn version 3.0
 ; LENGTH: 423
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-656-002-2

Query Match 27.2%; Score 665.5; DB 4; Length 423;
 Best Local Similarity 35.4%; Pred. No. 2.6e-56;
 Matches 160; Conservative 72; Mismatches 157; Indels 63; Gaps 16;

Qy 26 ISPVAADDAVAAQFQISLPLKFPIVIGIALLI-- -ALAATGLIHPDCSGKYRCRSS 82
 Db 9 VSPWRRBSEVSIPLIILASLAIIVVRLKIVLDKTYFLCQPLHF----- 56
 Qy 83 FKCIELIARCGVSPDKDGEDEYRC-----VRYGGQNAVLOVETAA-SWIKMC 129
 Db 57 --IPPKQLCIGELDPLGEDEHCKSKSPEGPAVARLISKDRSTLQVLDSDATGNWFSAC 113
 Qy 130 SDDWKGHAYNACAOQGFPSYVSSDNLRVSSLQGFRREEFVSTDHLPPDKVTAHLHSVY 189
 Db 114 FDNTFPAELAETAFCRONGIYSS----- -KTFTRAVEIGPHQDLDVETTENSEIR 161
 Qy 190 VREG-- -CASGHVYTLQCTAGHREGYSSRIVGEMMSLISOWPMQASLOFOGYHLCGSV 246
 Db 162 MRNSSGPCLSSLSVSHCLAG-KSLKTPRVGSEASYDSWPQVSIXDQHVCGESI 220
 Qy 247 ITPLWLTAAHCV-- -YDLXLPKSMTIQVGLVSLDNPAPSHLVKIV-- -YHSKVKPQR 300
 Db 221 LDPHWVLTAAECFRKHTDVF-- -NMKVRAGSDKL--GSFPLSLAVAKIIIIEFNMDY-PK-273
 Qy 301 LGNDIALMKLQAGPLFNFEMTOQVCLPNSEEFPDGKVKWTSGMGT-EGGDDASPVLNHA 359
 Db 274 -DNDIALMKLQFPLTHSGTVPICLPUFDELTPATPLWLTGNSFTKGMNSDILLQA 332
 Qy 360 AVPLISNKICNHRDYGGIIISPMSMLCAGYLTGGDSQGDSGGPLVCQERRLWKLVGATS 419

Query Match 27.4%; Score 669.5; DB 5; Length 98;
 Best Local Similarity 37.0%; Pred. No. 2.6e-56;
 Matches 146; Conservative 70; Mismatches 146; Indels 33; Gaps 14;

Qy 66 GLGIHFD-C-SGKTRCRSSRCIBIARCDGVSDCKDGEYRCVRV-- -GGNAVILQVF 120
 Db 415 GLGIPERCPEDNPKQKD-G-ECIPLVNLCDGPCKDSDAEAVRLNGTDSGLYQFR 473
 Qy 121 TAASWKTMCSDDKGHYANVACAGLGPSPYVSSDNLRVSLECGQFREBVSIDHLLPDDK 180
 Db 474 IQSIVMVAEENWTQISDVQCLGLGT-- -GNNSVPTFSTG-- -GPVNIN----- 521
 Qy 181 VTAHHHSVYY--REGCASHVVTLOCT--ACGHR--RGYSSRIVGNNMSLUSQWPAOS 233
 Db 522 -TAPNGSLILTPSQQCLESLILQCNYSCKKLTVQVSPKIVGSDREGAWPVVA 580

RESULT 14
US 09-000-846-2
Sequence 2, Application US/09000846
Patent No. 5981830

GENERAL INFORMATION
APPLICANT: WU, QINGYU
APPLICANT: SADLER, JASPER
TITLE OF INVENTION: KNOCKOUT MICE AND THEIR PROGENY WITH DISRUPTED SERINE PROTEASE GENES
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000, 846
FILING DATE: 30-DEC-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 800
ATTORNEY/AGENT INFORMATION:
NAME: LEBOVITZ, RICHARD M.
REGISTRATION NUMBER: 37, 067
REFERENCE/DOCKET NUMBER: BERLX 65P1
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US 09-000-846-2

Query Match Score 665; DB 2; Length 416;
Best Local Similarity 38.1%; Pred. No: 2.9e-56;
Matches 143; Conservative 54; Mismatches 136; Indels 42; Gaps 9;

Qy 100 DGEDEYRCYVGQNANVLOVF--TAASWIKMCSDDWKGHYANVAYAACQGFPSVYSSDNLR 157
Db 46 DQEPEPYQ-vQVQSPGSPRLAIVEDKTEGTWILCSSLRSNAVAGIICEEENGFLRALAHSELD 104

Qy 158 VSSLEGQFREEFVSD-----HLLPDDKVTALRHSHSYVREGCASASHVTLQCTAGH 209
Db 105 VRTAGANGTSGGFFCYDEGGJRLAQQLL-DVISYC-----DCPRGRFLATCDGGR 154

Query Match Score 658; DB 3; Length 435;
Best Local Similarity 35.7%; Pred. No: 1.5e-55;
Matches 158; Conservative 74; Mismatches 147; Indels 64; Gaps 18;

Qy 210 RGYSSRIVGGMNSLLSQWPWQASLQFGQGHLCGSVTPWLIITAACVYDLYLPK-- 266
Db 155 RKLPVDRVGGQDSSIGRWNQVSLRYDGTGTHLGCGSLLSGDWVLAHC----FPERNR 209

Qy 267 ---SWTIQGLYSLDNPAPSHLVKIVTHSKYKPKR-----LGNDIAALMKLAGPLTFN 317
Db 210 VLSRWRVEAGAVARTSPHAQOLGVAVITHGGYLFRDPTIDENSNDALVHSSLPLT 269

Qy 318 EMIQPVCPLNSEENFPDGKVWTSNGATEDGGDASPVLNHAAYPLISKICNHRDVYGG 377

RESULT 15
US-09-008-271A-6
Sequence 6, Application US/09008271A
Patent No. 6203919

GENERAL INFORMATION
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3114 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008, 271A
FILING DATE: 16-Jan-1998

PRIOR APPLICATION DATA:
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41, 201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLINNOF13
CLONE: 1337018

SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

US-09-008-271A-6

Query Match Score 658; DB 3; Length 435;
Best Local Similarity 35.7%; Pred. No: 1.5e-55;
Matches 158; Conservative 74; Mismatches 147; Indels 64; Gaps 18;

Qy 44 LPKPFPIVIGVIIAIIA-----IGLGIHFDQSGKVRCRSSFKC---IELIAR--- 91
Db 22 IPMETTRKVGPITIALLSASTIVVVLKVILD---KY---YFLCGQGPFLHF-PRKQL 74

Qy 92 CDGVSDKDGEDBEYR-----VRYGGQNAWLQVFTAA-SWKTMCSDDWKGHYA 138

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Db    75 CDGELDCPLGEDDEBCVKSFPPEGPAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALA 134
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Db    135 ETACRQMSYSS-----KPTRAVEGPDPQLDVYBTTENJSQERMBNSGPCL 182
Qy    196 SGHVVTLQCTACCHRRGYSRIVGNNSLSSPWAQSLQFGYHLGGSVITPMIITA 255
Db    183 SGSIVSLLHOLACGESEL-KPRVYIGGEASVDSWPWQSYIQLDKQHYCGGSILDPHWVLT 241
Qy    256 AHCV---YDLYLPKSWTIQVGLYSLDNPAPSHLVEKIV--YHSKYKPKRIGNDIALMK 309
Db    242 AKCPRKHTDVF--NWKVTRAGSDKL-GSFPSLAVAKIIIEBNPMY-PK-DNDIALMK 293
Qy    31.0 LAGPLTENEMIOPYCLPNSSENFPDGKWCWTSGMWAT-BDGDDASPVLNHAAPLISNKI 368
Db    294 LQFPLTFSTVRPCLPFFDEELTPATPLWIGWGFTKONGGKMSDLILLQASQVIDSTR 353
Qy    369 CNHRDVYGGIIIPSPMLCAGYLTTGGVDSCQGDSSGGPLIVCQERRLWKLVGAATFGIGCAEVN 428
Db    354 CNADAYQCEVTERMCAGIPEGVDTQGDSSGGPLMYQSDQ-WHYVGIVSWGYGGGPPS 412
Qy    429 KPGYXYTRTTSFLDWIHEQMERTL 451
Db    413 TPGYXTKV/SAYLNWIYNWKAEL 435

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Search completed: May 5, 2004, 15:49:26
 Job time : 23 secs

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	2443	100.0	453	10	US-09-999-830A-69	App1
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18	2443	100.0	453	10	US-09-978-187B-69	App1
19	2443	100.0	453	10	US-09-978-643A-69	App1
20	2443	100.0	453	10	US-09-976-191-12	App1
21	2443	100.0	453	10	US-09-978-375A-69	App1
22	2443	100.0	453	10	US-09-978-298A-69	App1
23	2443	100.0	453	10	US-09-978-188A-69	App1
24	2443	100.0	453	10	US-09-978-681A-69	App1
25	2443	100.0	453	10	US-09-978-194A-69	App1
26	2443	100.0	453	10	US-09-999-829A-69	App1
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29	2443	100.0	453	10	US-09-978-665A-69	App1
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31	2443	100.0	453	12	US-10-058-270A-60	App1
32	2443	100.0	453	12	US-10-164-749A-69	App1
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34	2443	100.0	453	12	US-10-199-670-64	App1
35	2443	100.0	453	12	US-10-201-858-64	App1
36	2443	100.0	453	12	US-09-999-031A-69	App1
37	2443	100.0	453	12	US-10-205-890-64	App1
38	2443	100.0	453	12	US-10-208-024-64	App1
39	2443	100.0	453	12	US-10-201-053-64	App1
40	2443	100.0	453	12	US-10-013-317A-63	App1
41	2443	100.0	453	12	US-10-174-581-64	App1
42	2443	100.0	453	12	US-10-176-481-64	App1
43	2443	100.0	453	12	US-10-176-49-64	App1
44	2443	100.0	453	12	US-10-176-914-64	App1
45	2443	100.0	453	12	US-10-176-914-64	App1

ALIGNMENTS

RESULT 1
US-09-978-295A-69
Sequence 69, Application US/09978295A
Patent No. US2002156006A1

GENERAL INFORMATION:

/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hansner
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillian, Kenneth J.
/ APPLICANT: Kjavian, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Par, James
/ APPLICANT: Pacini, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William T.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P630P1C1
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
DRAFTED DOCUMENT NUMBER: 00000000000000000000000000000000

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillian, Kenneth J.
APPLICANT: Kjavvin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paonni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumans, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OF INVENTION: Secred and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
ORIGIN: A DOCUMENT NUMBERED: 00-010555

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	2443	100.0	453	9 US-09-978-295A-69	Sequence 69, Appl1
2	2443	100.0	453	9 US-09-978-697-69	Sequence 69, Appl1
3	2443	100.0	453	9 US-09-978-192A-69	Sequence 69, Appl1
4	2443	100.0	453	9 US-09-999-832A-69	Sequence 69, Appl1
5	2443	100.0	453	10 US-09-978-189-69	Sequence 69, Appl1
6	2443	100.0	453	10 US-09-978-608A-69	Sequence 69, Appl1
7	2443	100.0	453	10 US-09-978-585A-69	Sequence 69, Appl1
8	2443	100.0	453	10 US-09-978-1912A-69	Sequence 69, Appl1
9	2443	100.0	453	10 US-09-978-403A-69	Sequence 69, Appl1
10	2443	100.0	453	10 US-09-978-564A-69	Sequence 69, Appl1
11	2443	100.0	453	10 US-09-999-833A-69	Sequence 69, Appl1
12	2443	100.0	453	10 US-09-981-191A-69	Sequence 69, Appl1
13	2443	100.0	453	10 US-09-978-824A-69	Sequence 69, Appl1
14	2443	100.0	453	10 US-09-918-585A-69	Sequence 69, Appl1
15	2443	100.0	453	10 US-09-918-585A-69	Sequence 69, Appl1
16	2443	100.0	453	10 US-09-918-585A-69	Sequence 69, Appl1

PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match Similarity 100.0% Score 2443; DB 9; Length 453;
 Best Local Similarity 100.0% Pred. No. 2.3e-225; Indels 0; Gaps 0;
 Matches 453; Conservative 0; Nismatches 0;

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Qy   1  MGENDPFAVEAPFSPRSFLGDDLKISPAVADAVAAQISSLPLKFPIIVIGIIL 60
Db   1  MGENDPFAVEAPFSPRSFLGDDLKISPAVADAVAAQISSLPLKFPIIVIGIIL 60
Qy   61  LALAIGIGHEDCGXCRSSFKCIELJARCDGYSDCKDGEDEYRCYRGGNNAVQF 120
Db   61  LALAIGIGHEDCGXCRSSFKCIELJARCDGYSDCKDGEDEYRCYRGGNNAVQF 120
Qy   121  TAASWKTMCSDWKGHYANACAOQGFPSYSSDNLRVSSLEGQFREEVSIIDHLPPDK 180
Db   121  TAASWKTMCSDWKGHYANACAOQGFPSYSSDNLRVSSLEGQFREEVSIIDHLPPDK 180
Qy   181  VITALHHSVYREGCASGHVTLQCPAGHRRGSSRIVGENMSLJSOWNQASLQFOGYH 240
Db   181  VITALHHSVYREGCASGHVTLQCPAGHRRGSSRIVGENMSLJSOWNQASLQFOGYH 240
Qy   241  LGGSVTTPLWITIAHCYDLYLPKSWT1QVGLVSLDNPASHLVKIVISKYKXR 300
Db   241  LGGSVTTPLWITIAHCYDLYLPKSWT1QVGLVSLDNPASHLVKIVISKYKXR 300
Qy   301  LGNDIALMKLAGPLTFNEMIQPVCLPNSSENFPGKVCNTSGWATEDGDSAPVNLHA 360
Db   301  LGNDIALMKLAGPLTFNEMIQPVCLPNSSENFPGKVCNTSGWATEDGDSAPVNLHA 360
Qy   361  VPLISNKICNERDVIGGIIPSMLCAQYLQGVDSQGDGGPLVYCQERRLWKLVGATSF 420
Db   361  VPLISNKICNERDVIGGIIPSMLCAQYLQGVDSQGDGGPLVYCQERRLWKLVGATSF 420
Qy   421  GIGCAVNPKPEVYTRTSFLDWHOMERDIKT 453
Db   421  GIGCAVNPKPEVYTRTSFLDWHOMERDIKT 453

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RESULT 2
 US-09-978-697-69
 Sequence 69, Application US/09978697
 Patent No. US2002016928A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillen, Kenneth J.
 APPLICANT: Kljatov, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paonni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tomas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William J.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 Acid Encoding the Same
 FILE REFERENCE: P2630PJC27
 CURRENT APPLICATION NUMBER: US/09/978-697
 CURRENT FILING DATE: 2001-10-16
 PRIOR APPLICATION NUMBER: 60/09/918585
 PRIOR FILING DATE: 2001-10-30
 PRIOR APPLICATION NUMBER: 60/06/62250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/06/6249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/06/5311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/06/63364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/07/7450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/07/7632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/07/7641
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 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/07/7791
 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 60/07/8004
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 PRIOR APPLICATION NUMBER: 60/07/8886
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 PRIOR APPLICATION NUMBER: 60/07/8936
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 PRIOR APPLICATION NUMBER: 60/07/89294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/07/9656
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 PRIOR APPLICATION NUMBER: 60/07/9663
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/07/9728
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/07/9786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/07/9920
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/08/0105
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/08/0107
 PRIOR APPLICATION NUMBER: 60/08/0165

PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-04-23
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PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
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PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084355
PRIOR FILING DATE: 1998-05-05

PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085519
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 9; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

Qy 1 MGENDPPAVEAPPSRSFLGDLDKLSPVAPDAVAQIQLSLPLKFPPIVIGIIALI
Db 1 MGENDPPAVEAPPSRSFLGDLKLSPVAPDAAAQIQLSLPLKFPPIVIGIIALI
61 LALAGLIGHEDDSKGXKPCBSSPKCIELIARCGSDCKDGEDEYTCVRYGQNAYLQVF 120
61 LALAGLIGHEDDSKGXKPCBSSPKCIELIARCGSDCKDGEDEYTCVRYGQNAYLQVF 120
Qy 12.1 TAAWKTMCSDDKGHANVACQGLGPFSYKSSDNLYSSLEGQFREEFVSYDHLIPDDK 180
Db 12.1 TAAWKTMCSDDKGHANVACQGLGPFSYKSSDNLYSSLEGQFREEFVSYDHLIPDDK 180
Qy 181 VTALHHSYTREGASGHVTLQCTACHRGGYSSRIVGGNSLSSMPWQSLSQFQGYH 240
Db 181 VTALHHSYTREGASGHVTLQCTACHRGGYSSRIVGGNSLSSMPWQSLSQFQGYH 240
Qy 241 LGCGSIVTPLWITTAHCYDYLPLKSWNTIOYGVLSSLDNPAFSHLYKEVTHSKYKPKR 300
Db 241 LGCGSIVTPLWITTAHCYDYLPLKSTNTQGLVSLIDNPAFSHLYKEVTHSKYKPKR 300
Qy 301 LGNDIALMCLAGPTENEMIQPVCLPNSEENFDGKVWTSGATEGDGDASPVLNHAA 360
Db 301 LGNDIALMCLAGPTENEMIQPVCLPNSEENFDGKVWTSGATEGDGDASPVLNHAA 360
Qy 361 VPLISNKICNHRDVGGIISPSMLCAGYLTTGGVDSQCDSGGPLVCQERRMLVGAATSF 420
Db 361 VPLISNKICNHRDVGGIISPSMLCAGYLTTGGVDSQCDSGGPLVCQERRMLVGAATSF 420
Qy 421 GIGCBNEVKPGVYTRVTSFLDWIHEQMERDLKT 453

D5 421 GIGCAEVNRPGVYTRVISFLDWTBQMERDLKT 453

RESULT 3
US-09-978-192A-69
Sequence 69, Application US/09978192A
PATENT NO. 60/079656

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillian, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pat, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ana
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.

TITLE OF INVENTION: Seeded and Transmembrane Polypeptides and Nucleic Acid Reference: P2610P1C9

CURRENT FILING DATE: 2001-10-15
CURRENT APPLICATION NUMBER: US/09/978,192A
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/162250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
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PRIOR APPLICATION NUMBER: 60/078936
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-04-29
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 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/055704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 9; Length 453;
 Best Local Similarity 100.0%; Pred. No. 2, 3e-225; Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGENDPVAEAPPFSRSLFGDDLKTSVAPDADAVAOISSLPLKFPIIVIGITALI 60
 Db 1 MGENDPVAEAPPFSRSLFGDDLKTSVAPDADAVAOISSLPLKFPIIVIGITALI 60

Qy 61 LALAIGIGIHDGCSGKYCRSSFKCTELARCDGYSDCDCDEBYRCVRGGQNAYQVF 120
 Db 61 LALAIGIGIHDGCSGKYCRSSFKCTELARCDGYSDCDCDEBYRCVRGGQNAYQVF 120

RESULT 4
 US-09-999-832A-69
 Sequence 69, Application US/0999832A
 Publication No. US20040192706A1
 GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eatori, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hansperger
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Godard, Audrey
 ; APPLICANT: Gradowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillian, Kenneth J.
 ; APPLICANT: Klijavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Par, James
 ; APPLICANT: Paon, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Sheldon, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William T.
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P26301C63
 CURRENT APPLICATION NUMBER: US/09/999, 832A
 CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/053111
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066364
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/077450

Query Match 100.0%; Score 2443; DB 9; Length 453;
 Best Local Similarity 100%; Pred. No. 2.3e-225;
 Matches 453; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MGENDPPAVEAPFSRSLFLGLDLKISPVAPADAYAQIISLPLKFFPIVIGIALL 60
 Db 1 MGENDPPAVEAPFSRSLFLGLDLKISPVAPADAYAQIISLPLKFFPIVIGIALL 60

Qy 61 LALAGLIGHFDSGKTRCSRSSFKC-ELIARDGSDDCKDSEDEPVCVRGGQANLVQE 120
 Db 61 LALAGLIGHFDSGKTRCSRSSFKCIELIARDGSDDCKDSEDEPVCVRGGQANLVQE 120

Qy 121 TARSWKTMCSDDMKGHYANVAQAQLGPSPYYSSDNLRVSLQDFREEFYSIDHLLPDK 180
 Db 121 TARSWKTMCSDDMKGHYANVAQAQLGPSPYYSSDNLRVSLQDFREEFYSIDHLLPDK 180

Qy 181 VITALHHSTVREGCAASGVITLQCTACGHRGGYSSRIVGGNMSLISQWPQASLQFGTH 240
 Db 181 VITALHHSTVREGCAASGVITLQCTACGHRGGYSSRIVGGNMSLISQWPQASLQFGTH 240

Qy 241 LGCGSVITPLWITAACVYDLYLPKSWTIVLGSLDNPASHLVEKLVHSKYKPKR 300
 Db 241 LGCGSVITPLWITAACVYDLYLPKSWTIVGLVSILDNPASHLVEKLVHSKYKPKR 300

Qy 301 LGNDIALMKLAGPLTENEMIQPYCLPNESENFPDGKVICWTSGWATEDGGDASPVLHAA 360
 Db 301 LGNDIALMKLAGPLTENEMIQPYCLPNESENFPDGKVICWTSGWATEDGGDASPVLHAA 360

Qy 361 VPLISNKICNRDVYGGI1SPSMILCAGYLTVGVDSCGDSGGPLVQERRLWKLVGATSF 420
 Db 361 VPLISNKICNRDVYGGI1SPSMILCAGYLTVGVDSCGDSGGPLVQERRLWKLVGATSF 420

Qy 421 GIGCAEVNRPGYTRVTSPLDWTHEQMERDLKT 453
 Db 421 GIGCAEVNRPGYTRVTSPLDWTHEQMERDLKT 453

RESULT 5
 US-09-978-189-69
 Sequence 69, Application US/09378189
 General Information:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Borstein, David
 APPLICANT: Destroyer, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Kliaviv, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napior, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann

PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081049
 PRIOR FILING DATE: 1998-04-08
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100 %; Score 2443; DB 10; Length 453;
 Best Local Similarity 100 %; Pred. No. 2.3e-225;
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGENDPDAVEAPPSFSPLGDDLKSPVAPDADAYAQILSLIPKFFPIVIGIALI 60
 Db 1 MGENDPDAVEAPPSFSPLGDDLKSPVAPDADAYAQILSLIPKFFPIVIGIALI 60

Qy 61 LALAIAGLIGHFDCSGYCRCSSFKCIELIARCDGVSDCKDGEDEYCRVRYGGONAVLQVF 120
 Db 61 LALAIAGLIGHFDCSGYCRCSSFKCIELIARCDGVSDCKDGEDEYCRVRYGGONAVLQVF 120

Qy 121 TAASWKTMCSDDWKGHYANVACAOQJGFPSVYSSDNIRVSSLEGQREFEYVSIDHLLPDDK 180
 Db 121 TAASWKTMCSDDWKGHYANVACAOQJGFPSVYSSDNIRVSSLEGQREFEYVSIDHLLPDDK 180

Qy 161 VTAALHHSVYVREGCASHVVTIQLCTAGHRRGYSSRIVGGNMSLSQWPQAISLQFGYH 240
 Db 161 VTAALHHSVYVREGCASHVVTIQLCTAGHRRGYSSRIVGGNMSLSQWPQAISLQFGYH 240

Qy 241 LCGGSVITPLWITIAHCVDYLPLKSWTIQVGLNSLDNPAPSHIVEKLYVSKYKPKR 300
 Db 241 LCGGSVITPLWITIAHCVDYLPLKSWTIQVGLNSLDNPAPSHIVEKLYVSKYKPKR 300

Qy 301 LGNDIAMKLQAPLTBNEMIQPVCLNSEENFPDGKWCNTSGWATEDGDDASPVLNHA 360
 Db 301 LGNDIAMKLQAPLTBNEMIQPVCLNSEENFPDGKWCNTSGWATEDGDDASPVLNHA 360

Qy 361 VPLISNIKICNRHDVYGGTISPMUCGYLTCGVDSDQGDSGCPVQERRLWKLNGATSF 420
 Db 361 VPLISNIKICNRHDVYGGTISPMUCGYLTCGVDSSQGDSCGPLYQERRLWKLNGATSF 420

Qy 421 GIGGAEVNPKGYTRVTSFLDMTHEQMERDLKT 453
 Db 421 GIGGAEVNPKGYTRVTSFLDMTHEQMERDLKT 453

RESULT 6
 US-09-978-608A-69
 Sequence 69, Application US/09978608A
 Publication No. US20030045462A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi

PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
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PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-13
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
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 PRIOR FILING DATE: 1998-05-15
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match Score: 100.0% / Score: 2443; DB: 10; Length: 453;
 Best Local Similarity: 100.0%; Pred. No.: 2, 3e-25;
 Matches: 453; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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Qy      1 MGENDPPAYEAPPFSRSLFGLDDDKRISPKVAPDAVAQIQLSLPLKFPPIVIGITALI 60
Db      1 MGENDPPAYEAPPFSRSLFGLDDDKRISPKVAPDAVAQIQLSLPLKFPPIVIGITALI 60
Qy      61 LALAIGLGHIFDCSGSKYRKCRSSPKCIELIARCDGVSDCKDGEDEYRCVRGGQNAYLQVF 120
Db      61 LALAIGLGHIFDCSGSKYRKCRSSPKCIELIARCDGVSDCKDGEDEYRCVRGGQNAYLQVF 120
Qy      121 TAASKPTMGSDDWIGHYANAVACAGLFPEYYSSPDNLRLVSLEQFREEPVSIDHLLPDK 180
Db      121 TAASKPTMGSDDWIGHYANAVACAGLFPEYYSSPDNLRLVSLEQFREEPVSIDHLLPDK 180
Qy      181 VTALEHHSVTYREGCASGHVTLQTAGCHRGYSSRIVGGMMSLQWQSLQFGYH 240
Db      181 VTALEHHSVTYREGCASGHVTLQTAGCHRGYSSRIVGGMMSLQWQSLQFGYH 240
Qy      241 LGGSVITPLWITIAAHCTDLYPKSWITIQGVLSLJUNPAFLVHVKIVYHSKYKPR 300
Db      241 LGGSVITPLWITIAAHCTDLYPKSWITIQGVLSLJUNPAFLVHVKIVYHSKYKPR 300
Qy      301 LGNDALMLKLAGPLTENM1QPVCLPNSBNFPQKVCWTSGVATEEGDASPVLNHA 360
Db      301 LGNDALMLKLAGPLTENM1QPVCLPNSBNFPQKVCWTSGVATEEGDASPVLNHA 360
Qy      361 VPLISNKINHRDYGIGIIPSMILCAGYLTGGYDSCOGSGPLVCOERLMLKVGATSF 420
Db      361 VPLISNKINHRDYGIGIIPSMILCAGYLTGGYDSCOGSGPLVCOERLMLKVGATSF 420
Qy      421 GIGCAEVNPKGVYTRVTSFLDWIHEQMERDLKT 453
Db      421 GIGCAEVNPKGVYTRVTSFLDWIHEQMERDLKT 453

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RESULT 10
 US-09-978-564A-69
 Sequence 69, Application US/09978564A
 Publication No. US0030050241A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Prior Application Number: 60/080194

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; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080331
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
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; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-16

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Query Match 100.0%; Score 2443; DB 10; Length 453;
 Best Local Similarity 100.0%; Pred. No. 2.3e-225;
 Matches 453; Conservative 0; N_mismatches 0; Indels 0; Gaps 0;

Qy	1	MGENDDPVAEAPFSPLGFLDDKISPVAPDADAVAAQILSLPLKFPIIVIGIALI	60
Db	1	MGENDDPVAEAPFSPLGFLDDKISPVAPDADAVAAQILSLPLKFPIIVIGIALI	60
Qy	61	LALAIGLIGHFDGSGKGRCSSEKCTELIARCDGVSCKDGDGEDEYCVRGQNAVLYQP	120
Db	61	LALAIGLIGHFDGSGKGRCSSEKCTELIARCDGVSCKDGDGEDEYCVRGQNAVLYQP	120
Qy	121	TRASWKTMCSDWKGHYANVACALQPFPSYSSDNLRRVSSLEGQFREFTSYIDHLLPDK	180
Db	121	TRASWKTMCSDWKGHYANVACALQPFPSYSSDNLRRVSSLEGQFREFTSYIDHLLPDK	180
Qy	181	VITALHHHSVYREGCASHVVTLOCTAGHRRGYSSPILVGNNNSLSQWPQOASLQFGYH	240
Db	181	VITALHHHSVYREGCASHVVTLOCTAGHRRGYSSPILVGNNNSLSQWPQOASLQFGYH	240
Qy	241	LCGGSVITPLWITTAACVYDYLPLPSWTICVGLVLLDPAPSHVEKIVYHSKKPKR	300
Db	241	LCGGSVITPLWITTAACVYDYLPLPSWTICVGLVLLDPAPSHVEKIVYHSKKPKR	300
Qy	301	LGNDIAIMKLAKPLTFNEMIQPVCLPNSEENFPDGRCWNTSGWGATEDGGDASPVLNHAA	360
Db	301	LGNDIAIMKLAKPLTFNEMIQPVCLPNSEENFPDGRCWNTSGWGATEDGGDASPVLNHAA	360
Qy	361	VPLISNKICNHRDVYGAIIISPMCLAGYLTCGAVDSQGDSGPLVQERRLMKLYGATSF	420
Db	361	VPLISNKICNHRDVYGAIIISPMCLAGYLTCGAVDSQGDSGPLVQERRLMKLYGATSF	420
Qy	421	GIGCAANPKGYTTRVTSFLDMTHEQMERDILT	453
Db	421	GIGCAANPKGYTTRVTSFLDMTHEQMERDILT	453

RESULT 11
 Publication No. US20030054405A1
 Sequence 69, Application US/09999833A
 General Information:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Oiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Sheiron, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William T.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630P165
 CURRENT FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
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 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
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 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079656
 PRIOR FILING DATE: 1998-03-26

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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 2443; DB 10; Length 453;
 Best Local Similarity 100.0%; Pred. No. 2,3e-228; Indels 0; Gaps 0;

Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGENDPPAVAPFSPRSFLGIDDKLISPVAPDADAVAAQILSLPLKFPPIVIGIALI 60
 Db 1 MGENDPPAVAPFSPRSFLGIDDKLISPVAPDADAVAAQILSLPLKFPPIVIGIALI 60
 Qy 61 LALAIGLGHEDCSGRYCRSSFKCIELARCDGVSDCDGEDEYRCYRGGNONAVLYF 120
 Db 61 LALAIGLGHEDCSGRYCRSSFKCIELARCDGVSDCDGEDEYRCYRGGNONAVLYF 120
 Qy 121 TAASIKTMCSDDWKGHAYANACQLGFPSYVSYSSDNLRVSLEGOFREEFVSDHLLPDDK 180

Db 121 TAASIKTMCSDDWKGHAYANACQLGFPSYVSYSSDNLRVSLEGOFREEFVSDHLLPDDK 180
 Qy 181 VITALHHSVTVREGAASHVYLQCTAACGHRGGSSRTVGGNNMSLSSOMPWOASLQFQGYH 240
 Db 181 VITALHHSVTVREGAASHVYLQCTAACGHRGGSSRTVGGNNMSLSSOMPWOASLQFQGYH 240
 Db 241 LGGSVITPLWITTAHCYDYLPKSWTQEVLSLIDNPASHLVPKSWTQEVLSLIDNPASHLVPK 300
 Qy 241 LGGSVITPLWITTAHCYDYLPKSWTQEVLSLIDNPASHLVPKSWTQEVLSLIDNPASHLVPK 300
 Qy 301 LGNDALMKLQAGPLTFNEMIQVCLPNSBNFPDGKVCTSGMATEDGGDASPVLNHA 360
 Db 301 LGNDALMKLQAGPLTFNEMIQVCLPNSBNFPDGKVCTSGMATEDGGDASPVLNHA 360
 Qy 361 VPLISNKICNHRDYYGGLSPSMICAGLITGVDSCQGDGGPLVCOPRLWLVUGATSF 420
 Db 361 VPLISNKICNHRDYYGGLSPSMICAGLITGVDSCQGDGGPLVCOPRLWLVUGATSF 420
 Qy 421 GIGCAEVNKEPGVYTRVTSFLDWFHQMERDLKT 453
 Db 421 GIGCAEVNKEPGVYTRVTSFLDWFHQMERDLKT 453

RESULT 12 US-09-981-915A-69
 Sequence 69, Application US/0981915A
 Publication No. US20030054986A1
 GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan
 / APPLICANT: Ferrara, Napoleon
 / APPLICANT: Filvaroff, Eileen
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Hillan, Kenneth J
 / APPLICANT: Kjavvin, Ivar J.
 / APPLICANT: Kuo, Sophia S.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James
 / APPLICANT: Paonil, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Sheldon, David L.
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William L.
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 / FILE REFERENCE: B26301C12
 / CURRENT APPLICATION NUMBER: US/09/981, 915A
 / PRIOR APPLICATION NUMBER: 09/18585
 / CURRENT FILING DATE: 2001-10-16
 / PRIOR FILING DATE: 2001-07-30
 / PRIOR APPLICATION NUMBER: 60/052250
 / PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-04-15
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; PRIOR FILING DATE: 1998-04-15

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PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score: 2443; DB 10; Length: 453;
 Best Local Similarity 100.0%; Pred. No. 2; 3e-22; Indels 0; Gaps 0;
 Matches 453; Conservative 0; Mismatches 0;

Qy 1 MGENDPPAYEAPPFSRSLRGLDDKISPAVAPDAVAAGILSLLPLKFPIIVIGIALL 60
 Db 1 MGENDPPAYEAPPFSRSLRGLDDKISPAVAPDAVAAGILSLLPLKFPIIVIGIALL 60
 Qy 61 LALATGLGHFDCSKYRCRSSFCIELARCDGVSDCDCDGEDEYRCVRGGONAVLQVF 120
 Db 61 LALATGLGHFDCSKYRCRSSFCIELARCDGVSDCDCDGEDEYRCVRGGONAVLQVF 120
 Qy 121 TAASKTMCSDDWKHYANVACAQLGFPSSYVSDNLRYSSLEGREFEVSIDHLLPDK 180
 Db 121 TAASKTMCSDDWKHYANVACAQLGFPSSYVSDNLRYSSLEGREFEVSIDHLLPDK 180
 Qy 181 VITALHHSVTRECCASGHVTLQTAGCERGKYSRIVGNMILLSQWFOASLQFCQH 240
 Db 181 VITALHHSVTRECCASGHVTLQTAGCERGKYSRIVGNMILLSQWFOASLQFCQH 240
 Qy 241 LGGSVITPOMITIAHCYDLYPKSWTIVQGLVSLDNPASHLVEKIVSKYPR 300
 Db 241 LGGSVITPOMITIAHCYDLYPKSWTIVQGLVSLDNPASHLVEKIVSKYPR 300
 Qy 301 LGNDIALMKLAGPLTFNEMIQPVCLPNSSENFPDGKVWTSNGATEDGDSPLVHAA 360
 Db 301 LGNDIALMKLAGPLTFNEMIQPVCLPNSSENFPDGKVWTSNGATEDGDSPLVHAA 360
 Qy 361 VPLISNKNICNRDVYGGIISPSMICALGYLTGGVDSCQGNSGGPLVCQERRWLKVLGATSF 420
 Db 361 VPLISNKNICNRDVYGGIISPSMICALGYLTGGVDSCQGNSGGPLVCQERRWLKVLGATSF 420
 Qy 421 GIGCAEVNKGPGVYTRYTSTLDWIHQMERDLKT 453
 Db 421 GIGCAEVNKGPGVYTRYTSTLDWIHQMERDLKT 453

RESULT 13
 US-09-978-824-69
 Sequence 69 Application US/09978824
 Publication No. US20030055216A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napis, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.

PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081049
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 2443; DB 10;
 Best Local Similarity 100.0% Pred. No. 2, 3e-22;
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MGENDPAAFPFSRSLFGDDLKISPKAPDADAVAOILSLPLKFFPIITVGIATI
Db	1 MGENDPAAFPFSRSLFGDDLKISPKAPDADAVAOILSLPLKFFPIITVGIATI
Qy	61 LALAIGLGIHEDCSYCRSSPKCIELTARCDGVSDCKDGEDEYRCYRGGNONAVLQF
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Qy	121 TAASMTMCDDWMKHAYANAYACAQLGEPSPSYSSDNLYRVSLEQOFREBFVSIHDLLPDK
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Qy	181 VTAHLHSVTVREGCASHVVTLOCTAGHRRGYSSRIVGNNMLLSQNPWQAQLQGQYH
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Qy	241 LGGSVITPLWIIIAHCYDLYLPKSWTIQVGLVSLLDNPASHLVEKIVYTSKYKPKR
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Qy	301 LGNDIAMLKLAGPLTNEMIQPVCULPNSBNFPDKVCTSGMATEDGDAFPVLHAA
Db	301 LGNDIAMLKLAGPLTNEMIQPVCULPNSBNFPDKVCTSGMATEDGDAFPVLHAA
Qy	361 VPLISKICHNRDYYGGITSPSMICAGYLTTGGDSCQGDGGPLVYCQERRLWKLVGATSF
Db	361 VPLISKICHNRDYYGGITSPSMICAGYLTTGGDSCQGDGGPLVYCQERRLWKLVGATSF
Qy	421 GIGCAVNKGCVYTRVTSFLDWHEQMERDLKT 453
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RESULT 14 US-09-918-585A-69
 Sequence 69, Application US/0918585A
 Publication No. US2003006046A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Fong, Wei-Qiang
 APPLICANT: Pilvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
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 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
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 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2330P1C1
 CURRENT APPLICATION NUMBER: US/09/918,585A
 CURRENT FILING DATE: 2001-07-30

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 Best Local Similarity 100.0%; Pred. No. 2, 3e-22;
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 LALAIGLGHEDCSGKYRCRSSFKCIELARCDSGVDCCDGEDEYRCVRGGONAVQFV 120

Qy 121 TAASWKTMSIDWKGHAYANACAAQGFPSVYSSDNLRVSELEGOFREEFVSDHLLPDK 180
 Db 121 TAASWKTMSIDWKGHAYANACAAQGFPSVYSSDNLRVSELEGOFREEFVSDHLLPDK 180

Qy 181 VITALHHSVYREGCASGHVYTLQCTAGHRRGYSRIVGNNMSLQWASLQFGQYH 240
 Db 181 VITALHHSVYREGCASGHVYTLQCTAGHRRGYSRIVGNNMSLQWASLQFGQYH 240

Qy 241 LGGSVITPLMIIATAHCVYDLYLPLKSWT1QVGLYSLNPNASHLVKIVHVKYKR 300
 Db 241 LGGSVITPLMIIATAHCVYDLYLPLKSWT1QVGLVSLNPNASHLVKIVHVKYKR 300

RESULT 15
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 ; Sequence 69, Application US/09978423A
 ; Publication No. US20030069178A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Boistestein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
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 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William J.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; Acid Encoding the Same
 ; CURRENT APPLICATION NUMBER: US/09/978-423A
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Search completed: May 5, 2004, 15:54:14
 Job time : 49 secs

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Db	350 QGDGGPFTCEDJSISRTPRWRLLGIVSNTGCLAAQPKGTYTKVSDREWIFQAII 405	Qy	181 VITALHHSTVV---REGCAGSHVTLQCT--ACGHR---RGYSRIVGGNMNSLSQWPQAS 233	
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Proc. Natl. Acad. Sci. U.S.A. 91: 7588-7592, 1994		Db	878 IVINPHYNGRKCONDIAAMHLEMVKVNTDYLQICLPPENQVPPGRCISTAGWGLIYQ 937	
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A;Reference number: A41090		Db	938 GSTADVLOPADVPLNSEACQQQMPEN--ITINMVQZGYEAQGVDSQGDGGPLVQCE 995	
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A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ		Db	996 NNRWILLAGTVTSFGYQCALPNRPGYAYARVPRFTEWI 1030	
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A;Experimental source: small intestine		Qy	A56318 Enteropeptidase (EC 3.4.21.9) precursor [validated] - human	
R;Jiavallie, E.R.; Rehantka, A.; Racine, L.A.; DiBlasio, E.A.; Ferenz, C.; Grant, K.L.;		Db	N;Alternate names: enterokinase C;Species: Homo sapiens (man) C;Accession: GB:U09860; PMID:9746412; PID:9746413 C;Cross-references: GB:U09860; PMID:9746412; PID:9746413 R;Kitamoto, Y.; Veile, R.A.; Denis-Keller, H.; Sadler, J.E.	
J. Biol. Chem. 268, 23311-23317, 1993		Qy	C;Comment: The mechanism of association with the membrane of the intestinal brush border A;Note: parts of this sequence, including the amino end of the mature protein, were confirmed by Light, A.; Janska, H., 1995 J. Protein Chem. 10, 475-480, 1991	
A;Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of bovine enterokinase.		Db	A;Title: Enterokinase, the initiator of intestinal digestion. A;Reference number: A41090; PMID:94328561; PMID:805624 A;Accession: A56318; PMID:95234679; PMID:7718557 A;Molecule type: mRNA A;Residues: 801-1035 <LAV> A;Cross-references: GB:U19663; PMID:9416131; PMID:AAA16035.1; PID:9416132 A;Note: parts of this sequence, including the amino end of the mature protein, were confirmed by Light, A.; Janska, H., 1995 J. Protein Chem. 10, 475-480, 1991 A;Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase. A;Reference number: A61436; PMID:92189715; PMID:1793406 A;Accession: A61436 A;Molecule type: protein A;Residues: 801-801, Y, 809-827 <LIG>	
R;Kitamoto, Y.; Veile, R.A.; Denis-Keller, H.; Sadler, J.E.		Qy	A;Comment: The mechanism of association with the membrane of the intestinal brush border C;Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protein C;Complex: conversion from membrane-bound to soluble forms may involve further processing C;Function: cleaves propeptide from trypsinogen to produce active trypsin A;Pathway: intestinal digestive cascade C;Pathway: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding repeat C;Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protein P;22-38/Domain: transmembrane #status predicted <TM> P;52-117/Product: enteropeptidase heavy chain #status predicted <HCH> P;18-800/Product: enteropeptidase heavy chain #status predicted <HCH> P;358-520/Domain: LDL receptor ligand-binding repeat homology <LDL1> P;542-647/Domain: MAM homology <MAM> P;659-693/Domain: C1r/C1s repeat homology <C1R> P;694-799/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC> P;801-1035/Product: enteropeptidase light chain #status predicted <LCH> P;116-236/Domain: LDL receptor ligand-binding repeat homology <LDL2> P;841-892/987/Active site: His, Asp, Ser #status predicted	
F;643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2>		Qy	A;Description: cleaves activation peptide from trypsinogen to produce active trypsin A;Pathway: intestinal digestive hydrolytic cascade C;Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding repeat C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen F;184-221/Domain: transmembrane #status predicted <TM> F;22-38/Domain: transmembrane #status predicted <HCH>	
F;342-504/Domain: MAM homology <MAM>		Db	C;Function: cleaves activation peptide from trypsinogen to produce active trypsin A;Pathway: intestinal digestive hydrolytic cascade C;Superfamily: enteropeptidase; C1r/C1s repeat homology <LDL2>	
F;526-631/Domain: C1r/C1s repeat homology <C1R>		Qy	F;643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2> F;678-783/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC> F;785-1019/Product: enteropeptidase light chain #status predicted <LCH>	
66 GLGTHEDC-SGKYCRSSPKCIELJARCDGVSQDKDGEDEYRCVRY---GGONAVLQVF 120		Db	F;785-1019/Product: enteropeptidase light chain #status predicted <LCH>	
652 GLGIPPKCKDNFQCKDGB-BCIPVNLCKDFHKCDGSBAHCVRLFGTDDSGLQFQR 710		Qy	F;116-147, 19-328, 335, 388, 440, 470, 503, 534, 630, 682, 706, 725, 848, 887, 909, 949/Binding site: C	
121 TAASKTMCSDMKGHYANVACQLGPFSPYVSSDNLRLVSQLEQFREEVSDIHDLLDDK 180			F;772-896, 810-926, 910-977, 941-956, 967-995/Disulfide bonds: #status predicted F;825, 876, 971/Active site: His, Asp, Ser #status predicted	

Query Match Score 664.5; DB 1; Length 1019;
 Best Local Similarity 37.5%; Pred. No. 2, 9e-45;
 Matches 147; Conservative 67; Mismatches 149; Indels 29; Gaps 14;

Qy 67 LGIHFDCC-SGKYRCRSSFKCIELIARDGVSPCKDGDEYRCVR---VGGQNAVLOVFT 121
 Db 637 LGIPEPKEDNFQCENG-ECVLVNLCDGFSHCKGDSDEAHCYFLGNTANNSGLVFR 710
 Qy 122 AASWKTMCSDDMKGHYANVACAOGLFBSYSSDNLRSSLEGQFREFEVSIDHLLPDKV 695
 Qy 636 QSIWHTAACENWTQISDVCQULGLGSNSSK--PIFSTDG---GFVKL-NTAQDG-- 747
 Db 182 TALHHSVYREGGASGHVVTIQLCT--ACGHR --RGYSSRIVGGMNSLQWPAQSLQF 236
 Db 748 ---HLILTPSQCLQDSLIRLQNCNHSCKKLAADQITPKVGGSNAKEGMPWVGLYX 804
 Qy 237 QGYHLCGSSSVITPLWITAHCYDYL-PKSNTIQVGL--VSLLDNP-AASHLVKEIY 292
 Db 805 GGRULCGASLSSDWLVAACVYGRNLEPSKWTAILGHMKSNLTSPOVTPRLIDEV 864
 Qy 293 HSXKYPKRIGNDIALMKLAGPLTENIQPVCLPNSEBNFPDGKWCNTSGNGATEDGDA 352
 Db 865 NPHYMRKKNDIAMDMLLEKVNNTDYIQPICLPEENQFPGRNCSIAHGTVVYQGT 924
 Qy 353 SPVLNHAAPLISKINCHR-DVYGGTIPSMSLICAGYLGTGVDYNSCOGDGGPPLYCERR 411
 Db 945 ANLQEADPPLSNERCOCOMPENY-ITENMICAGYEEGGIDSCQDSGGPLMCENNR 982
 Qy 412 WKLVGATSGIGCAEVNKGYVRYTSPFLDWI 443
 Db 983 WFLAGVTTSGYKCALPNREGVYARVSRETEWI 1014

RESULT 4
 AS1663 enteropeptidase (EC 3.4.21.9) precursor [validated] - pig
 N: Alternate names: enteropeptidase
 C: Species: *Sus scrofa domesticus* (domestic pig)
 C: Accession: A53663
 C: Note: parts of this sequence, including the amino ends of three chains isolated from intestinal brush border of the membrane of the heavy chain. Orotate below or with amino-terminal myristoylation reported to contain two (heavy and light) chains. Possibly conversion from membrane-bound to soluble forms involved.
 C: Function: cleaves activation peptide from trypsinogen to produce active trypsin
 A: Cross-references: GB:D30799; PID:BAR06459.1; PID:9505123
 A: Pathway: intestinal digestive hydrolase cascade
 C: Superfamily: enteropeptidase
 C: Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
 F: 52-17/Product: enteropeptidase mini chain #status predicted <MCH>
 F: 52-18-799/Product: enteropeptidase heavy chain #status predicted <HCH>
 F: 119-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F: 357-519/Domain: MAM homology <MAM>
 F: 658-692/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F: 693-793/Domain: scavenger receptor cysteine-rich domain homology <LDL2>
 F: 800-1034/Domain: enteropeptidase light chain #status predicted <LCH>
 F: 800-1039/Domain: trypsin homology <TRY>
 F: 116, 147-170/Domain: trypsin homology <TRY>
 F: 87-911, 925-992/Domain: Disulfide bonds: #status predicted
 F: 840, 891, 985/Active site: His, Asp, Ser #status predicted

Query Match Score 663.5; DB 1; Length 1034;
 Best Local Similarity 37.8%; Pred. No. 3, 5e-45;
 Matches 149; Conservative 65; Mismatches 147; Indels 33; Gaps 14;

Qy 67 LGIHFDCC-SGKYRCRSSFKCIELIARDGVSPCKDGDEYRCVR---VGGQNAVLOVFT 121
 Db 652 LGIPEPKEDNFQCENG-ECVLVNLCDGFSHCKGDSDEAHCYFLGNTANNSGLVFR 710
 Qy 122 AASWKTMCSDDMKGHYANVACAOGLFBSYSSDNLRSSLEGQFREFEVSIDHLLPDKV 181
 Db 711 QSIWHTAACENWTQISDVCQULGLGTGNSSMPF-TSSGGG---EFVKLN----- 757
 Qy 182 TALHHSVYREGGASGHVVTIQLCT--ACGHR --RGYSSRIVGGMNSLQWPAQSL 234
 Db 758 TAPNGSLITTAEOCFSLSLILQCNTHSGKXQVAEVSPKVKVGDNSREGAWPNTVAL 817
 Qy 235 QFGQYHLCGSSVITPLWITAHCYDYL-PKSNTIQVGL--VSLLDNP-APSHLYVEI 290
 Db 818 YNGOLLCASLVSRDWLVSAACVYGNLEPSKWAIGLERTSNTSPQIVTRLDEI 877
 Db 291 VYHHSKYPKRIGNDIALMKLAGPLTENIQPVCLPNSEBNFPDGKWCNTSGNGATEDDG 350
 Db 878 VINPHYNRKRDSDIAAMHLEFKVNNTDYIQPICLPEENQFPGRNCSIAHGTVVYQ 937
 Qy 351 DASPVLNHAAPLISKINCHR-DVYGGTIPSMSLICAGYLGTGVDYNSCOGDGGPPLYC 409
 Db 938 SPADLQEADPPLSNERCOCOMPENY-ITENMICAGYEEGGIDSCQDSGGPLMCLEN 995
 Qy 410 RLWKVGATSGIGCAEVNKGYVRYTSPFLDWI 443
 Db 996 NRWLQAGTSGYKCALPNREGVYARVSRETEWI 1029

RESULT 5
 S33777 hepsin (EC 3.4.21.-) - rat
 C: Species: *Rattus norvegicus* (Norway rat)
 C: Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
 R: Farley, D.; Raymond, F.; Nick, H.
 Biochim. Biophys. Acta 1173, 350-352, 1993
 A: Title: Cloning and sequence analysis of rat hepsin, a cell surface serine protease.
 A: Reference number: S33777; MUID:93305733; PMID:8318746
 A: Accession: S33777
 A: Status: Preliminary
 A: Molecule type: mRNA
 A: Cross-references: EMBL:X70900; NID:957928; PID:CAA50256.1; PID:957929
 C: Superfamily: hepsin; trypsin homology
 C: Keywords: hydrolase; liver; serine proteinase; transmembrane protein
 F: 162-399/Domain: trypsin homology <TRI>
 F: 187-203 290-358 321-337,348-380/Disulfide bonds: #status Predicted
 F: 202,256/352/Active site: His, Asp, Ser #status Predicted

Query Match Score 654.5; DB 1; Length 416;
 Best Local Similarity 35.3%; Pred. No. 6, 4e-45;
 Matches 146; Conservative 61; Mismatches 156; Indels 51; Gaps 10;

Qy 60 ILAIAIGLTHFDCCSGYKRCRSSFKCIELIARDGVSPCKDGDEYRCVRGGMNSLQWV 119
 Db 17 VAALTVGTLFLTGIG---AASVAVTILLR-----SDQELVYQVSPGDSRLV 65
 Qy 120 -PTAAWKTMCSDDKHKGHYANVACAOGLFBSYSSDNLRSSLEGQFREFEVSID- 173
 Db 66 DKTEGWRWLQSSRSNARYAGLCEEMGFLRAHSELDVRAANGTSFFCVDEGGILP 125
 Qy 174 --HLPDDCUTAIHHSVYREGGASGHVVTIQLCTACGHRGYSRSTIUGNMSSLQWV 230
 Db 126 LAQRIL--DVTSVC-----DCPGRFPTATCQDGCRKLPLTDIVQGDSSLGRNW 175
 Qy 231 QASLQFQGHILCGGSVITPMWITAAHCYDYLQPK----SWTIQGVLSLLDNPAPS 284

QY 224 LLSQPKWQASLQFQ--GTHLGGSVITPLWITAHHCVYDLYPKSWTIQVGLSV--L 278
 Db 398 SLGEWPWQISLQVQLVSQTHLGGSIIIGRQWVTAHHCDGTYPDWRYGGILSSEI 457
 Qy 279 DNPASHLIVKIVHSSKYPKRLGNDIAMKLAGPLTNEMIQPVCPLPNSSEENPPDGKVC 338
 Db 458 TKEPESSRKELIITHQEYKVSEGNDIAIKLQPLNTYEFQRPICLPSKADNTTITNC 517
 Qy 339 WTSWGKATEDGGDASPVLNAAPLISNICK-NHRDVGCGIISPMSMLAGYLTTGGYDSC 396
 Db 518 WWTGMYGTYRQEGETONILQKATIPVNPBECOKYRD--VINKOMTCAG7KEGGTDAc 574
 Qy 397 QGDSSGCPVQERWRKLVGATSLIGVAEVNKGTVITVTSDFLDWLRHQME---RDLK 452
 Db 575 KGDGGGPVWCKHSGRWQVQGATTSWEGCCRKDQFGVYTKVSEIMDWILEKTQSSDVALE 634
 Qy 453 T 453
 Db 635 T 635

RESULT 9

KOUP

Plasma kallikrein (EC 3.4.21.34) Precursor - human

N;Alternate names: kininogen; Plasma prekallikrein
 ;Species: Homo sapiens (man)
 ;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
 C;Accession: A00921; A37339
 R;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
 Biochemistry 25, 2410-2417, 1986
 A;Title: Human plasma Prekallikrein, a zymogen to a serine protease that contains four t.
 A;Reference number: A00921; MUID:3524359; PMID:3521732
 A;Accession: A00921
 A;Molecule type: mRNA
 A;Residues: 1-618 <CHU>
 A;Cross-references: GB:M13143; NID:919062; PIDN:AAA60153-1; PID:g190263
 R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
 Biochemistry 30, 2050-2056, 1991
 A;Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of
 A;Reference number: A37930; MUID:9152016; PMID:198666
 A;Accession: A37939
 A;Molecule type: protein
 A;Residues: 20-27-46, X', 48, 'H', 50, 'X', 52-70, 'H', 75-76, 'X', 78-80, 103-113; 131-140; 141-
 1260-233, 'X', 285-287-291, 'X', 293-295-314-317, 'X', 319-320, 'X', 329-333; 334-339, 'X'
 55-538-551-562, 'X', 564-567-573, 'X', 575-576, 578-583, 'X', 585-592-604 <MCMB>
 C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex w
 are linked by one or more disulfide bonds.
 C;Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciprocal r
 inogen and may also play a role in the renin-angiotensin system by converting prorenin i
 C;Genetics:
 A;Gene: GDB:KLK3
 A;Cross-references: GDB:127575; OMIM:229000
 A;Map position: 4q35-4q35
 C;Superfamily: coagulation factor XI; trypsin homology
 C;Keyword: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; inflam
 P;1-19/Domain: signal sequence #status Predicted <SIG>
 P;20-239/Domain: plasma kallikrein heavy chain #status Predicted <MAT>
 P;20-638/Domain: plasma kallikrein light chain #status Predicted <LCH>
 P;20-108/Domain: apple repeat <AP1>
 P;110-199/Domain: apple repeat <AP2>
 P;200-389/Domain: apple repeat <AP3>
 P;291-380/Domain: apple repeat AP4

 F;391-621/Domain: trypsin homology <TRY>
 F;1-104,47-77,51,57,111-194,117-166,141-147,201-284,227-256,231-237,292-375,322-328,383
 F;127,308,396,453,494/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;318-347,340-345/Disulfide bonds: #status Predicted
 F;390-391/Cleavage site: Arg-IIe (coagulation factor XIIa) #status predicted
 F;434,483,578/Active site: His, Asp, Ser #status predicted

Query Match

Best Local Similarity 22.6%; Score 553; DB 2/6; Length 855;

Matches 135; Conservative 31.5%; Fred. No. 2.e-16; Indels 82; Gaps 15;

Db 453 CPGMEMCCTG-RCIRKDRCGWADCPSDPRHC-----RCNATHQFMCKNQ 499

Qy 73 CSGKYRERSSFKCIELTARDGVSDKEDGEDEYRCVRRGQNAVILQVFTASWKTMCSDD 132

Db 453 CBDEEGCSCPAGSFK--CSDEEGCSCPAGSFN-DCGD-----GSDDEGCFWYCDSYN-DCGD-----CSNGKCLPQSQQCNGKD 548

Qy 179 -----DKVTAHLHSYYVREGGASGHVVTLCTACGHRGGYs----- 214

Db 549 DCGDSDEASCDNVNAVSIKTYR-CQNLGLCNKNCEDGKKRCDSDERKNCDCGIL 607

Qy 133 -----WRGHYANVACAQLGFPSVYSSDNLVSSQEGQFREFVSLDHLLPD----- 178

Db 500 PCKPLFWYCDSYN-DCGD-----GSDDEGCFWYCDSYN-DCGD-----CSNGKCLPQSQQCNGKD 548

Qy 215 -----SPTKQARRGGTNADEGGMPWQVSLHALGOHHLGASL1SPDWLVSAAHCQDETIFKTS 667

Db 608 SPTKQARRGGTNADEGGMPWQVSLHALGOHHLGASL1SPDWLVSAAHCQDETIFKTS 667

Query Match Score 549.5; DB 1; Length 638;
 Best Local Similarity 35.8%; Fred. No. 2.e-36;
 Matches 124; Conservative 57; Mismatches 116; Indels 49; Gaps 11;

132 DWKCHYANVACAQLGFPSVYSSDNLVSSQEGQFREFVSLDHLLPD----- 179

RESULT 10
 JCF759 brain-specific serine proteinase (EC 3.4.21.-) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 31-Mar-2000
 C;Accession: JC5759
 C;Keywords: Glycoprotein; hydrolase; serine proteinase
 F;1-157/Domain: kringle-like #status predicted <KR>
 F;1-163/Domain: scavenger receptor cysteine-rich domain homology <SRC7>
 F;1-266/Domain: 386-416/Domain: furin binding #status predicted <FBB>
 F;1-513-516/Domain: trypsin homology <TR>
 F;93-521/569/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;562,612,711/Active site: His, Asp, Ser #status predicted

Query Match 21.6%: Score 527; DB 2; Length 761;
 Best Local Similarity 31.9%; Pred: No. 2 3e-34;
 Matches 14; Mismatches 53; Indels 118; Gaps 21;

Qy 70 HFD-----CSGKYCRRSSFKCTELIARCDGVSDCKGED-----103
 Db 326 HFDGSNRPINWLDVSSGK--EVSEF--TCSRWGRHDCSHREBDVGTCYPPDSGHRL 380

Qy 104 --EYRCVRGGQN--AVLQVFTAASWKTMCSDDWKGHYANVACAQLGP-----SY 150
 Db 381 SPGFPIRLDGENKEGRVEVFNGCQGTCDDGWTDKRAAVICRQLGTKGPARARTMAY 440

Qy 151 -----VSSONLRVSSLEQFREEEVSIHLLPDKVTALHHSV-----YREGCIS 196
 Db 441 FEGEGKSPHIMVNVKCTG----NEKALADCVQDGRIGNCRHESEDAGTYCDLEKRAAS 494

Qy 197 GHVVTLQCTAC---HRGYSRIVGGNSSLQOMPWAQSLOQGYH----LGGSVVI 247
 Db 495 SGNKEMLSGGCLRLHRR-QKRIGGANSLRGAWPKQASLRLRSAHDGRJLUGATL 552

Qy 248 TPLWIIITAHCYV-----YDLYLPKSWTIQVGLVSLDNPAFSLVKEIV 291
 Db 553 SSCWVLTAAHCFKRYGNNSRSYAVRGDHTLVPEEEQFEG-----VQQTIV 599

RESULT 11
 A61545 plasmin (EC 3.4.21.7) precursor - horse (fragments)
 N;Alternate names: Plasminogen
 N;Contain: miniplasminogen
 C;Species: Equus caballus (domestic horse)
 C;Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
 C;Accession: A61545; S1-7527
 R.Schaller, J.; Rickli, E.E.
 Enzyme 40, 63-69-1988
 A;Title: Structural aspects of the plasminogen of various species.
 A;Reference number: A61545; MUID: 89005015; PMID: 318975
 A;Accession: A61545
 A;Molecule type: protein
 C;Superfamily: Plasmin; kringle homology; plasminogen-related protein precursor homology;
 C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z;
 A;Residues: 1-33-34-117 <SC1>
 P;1-33/Domain: activation peptide (fragment) #status experimental <APT>
 P;1-33/Domain: plasminogen (fragment) #status experimental <MAT>
 P;37-114/Domain: kringle homology <KR4>
 P;118-455/Domain: miniplasminogen #status experimental <MIN>
 P;126-455/Domain: kringle homology <KR5>
 P;226-448/Domain: plasmin B #status experimental <BCB>
 P;226-448/Domain: trypsin homology <TR>
 F;267,310-405/Active site: His, Asp, Ser #status predicted

Query Match 21.5%: Score 526; DB 2; Length 455;
 Best Local Similarity 21.0%; Pred: No. 1.5e-34;
 Matches 107; Conservative 47; Mismatches 87; Indels 14; Gaps 6;

Qy 203 OCTA----CG----HRGYSRIVGGNSSLQOMPWAQSLOQFO-GYHLGGSVITPLWII 253
 Db 204 QCESSPDGKPKVTPKCSGRIVGCVTAHSNEWQISLRTGRHPFGGTLLISPENVL 263

Qy 254 TAAHCYDYLPKSMWNTIQGIVLSDNPASHLYVEKIVTHSKYKPKRGNNDIAIMKLAGP 313
 Db 264 TAAHCYDYLPSPTVFLGTHPHELRIAAGAQQI--VSKLFLERSA-DIALIKLSSP 319

Qy 314 LTENEMIQPVCLPNSSENFPDGKVWTSQNGATEDGGDASPVLNAVPLISNKICHNRD 373
 Db 320 AITTONVIPACLPPADYXVANWAECVTGEGTQDSNAG-VLKEAQLPVENKVCRNRY 378

Qy 374 VGGITSPSMECAGYLTGGVTDQGDSQGSGGLVQPERILWLGATSFGIGCAEVNPKPGYY 433
 Db 379 YLNGRKVSTELCAGHLYVGVDQGSGPLVUCFEDKYLQGTVSWGLGCARPNPKGYY 438

Qy 434 TRVTFILDWIHQME 448
 Db 439 VRVSSFINWIERIMQ 453

RESULT 12

Plasmin (EC 3.4.21.7) precursor - pig (fragment)
 N:Alternative names: Plasminogen
 N:Contains: miniplasminogen
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 07-Sep-1990 #sequence revision 01-Nov-1996 #text_change 18-Jul-1997
 C:Accession: S03733; S03737; A25834
 C:Accession: J.; Marti, T.; Roessel, S.J.; Kaempfer, U.; Rickli, E.E.
 Rischallier, J.; Marti, T.; Roessel, S.J.; Kaempfer, U.; Rickli, E.E.
 Fibrinolysis 1, 91-102, 1987
 A:Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the carboxyl-terminal CNBr fragments of human, porcine and bovine plasminogen.
 A:Reference number: S03735; MUID:81212097; PMID:7238497
 A:Accession: S03733
 A:Molecule type: Protein
 A:Residues: 1-550 <SCH>
 A:Residues: 1-550 <BRU>
 A:Residues: 1-57 <BRU>
 R.Marti, T.; Schallier, J.; Rickli, E.E.
 Eur. J. Biochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, porcine and bovine plasminogen.
 A:Reference number: A25834; MUID:85203907; PMID:3646533
 A:Accession: A25834
 A:Molecule type: protein
 A:Residues: 450-190 <MAR>
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of physiological processes; activates the urokinase-type plasminogen activator on the walls of the Graafian follicle; also activates the urokinase-type plasminogen activator pathway: fibrinolysis
 C:Superfamily: Plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine protease
 F:1-790/Product: Plasminogen #status predicted <PRO>
 F:1-790/Domain: Plasminogen-related protein precursor homology (fragment) <PLPH>
 F:1-77/Domain: activation peptide #status predicted <AP>
 F:1-77/Domain: activation peptide #status predicted <ACT>
 F:1-77/Domain: plasmin chain A #status predicted <ACH>
 F:1-77/Domain: plasmin chain B #status predicted <BCH>
 F:1-66-243/Domain: kringle homology <KR1>
 F:256-333/Domain: kringle homology <KR2>
 F:358-435/Domain: kringle homology <KR3>
 F:440-790/Product: miniplasminogen #status experimental <MIN>
 F:461-544/Domain: kringle homology <KR5>
 F:561-783/Domain: plasmin chain B #status experimental <BCH>
 F:561-783/Domain: tryptic homology <TRY>
 F:30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305-324/Domain: #status predicted
 bonds : #status predicted
 F:602,645,740/Active site: His, Asp, Ser #status predicted
 Query Match 21.4%; Score 523.5; DB 1; Length 790;
 Best Local Similarity 41.4%; Prod. No. 4.6e-34; Indels 21; Gaps 6;
 Matches 108; Conservative 43; Mismatches 89;
 Qy 194 CASGHVVTLQCTACGHRGGYSSRIVGGNNNLLSQWPWQIISLRY-YRGHFCGTLSPEN
 Db 547 CGKEKVEPKXCPA-----RIVGGCVTIPSPWQIISLRY-YRGHFCGTLSPEN 596
 Query Match 21.4%; Score 523.5; DB 1; Length 790;
 Best Local Similarity 41.4%; Prod. No. 4.6e-34; Indels 21; Gaps 6;
 Matches 108; Conservative 43; Mismatches 89;
 Qy 252 ITAAHCYVDLYLPKSWTIQVGLVSLQDNPAQSHLVECI-YVHSKYKPKRLGNDIALMK 309
 Db 597 VLTAGHCKLEKSSPSASYK-----ILGAHEEYTHLGEGVQEIVVSKLFKEPEADALLK 650
 Query Match 21.4%; Score 523.5; DB 1; Length 790;
 Best Local Similarity 41.4%; Prod. No. 4.6e-34; Indels 21; Gaps 6;
 Matches 108; Conservative 43; Mismatches 89;
 Qy 310 LAGPLTENEMIQPVCLPNSEENFPDGKVWTSGNGATEDGGDASPLVYAYPLNSKIC 369
 Db 651 LSPAVITDKVIAPLPTPNVVADETRACTIVTGEGTK-GTYAGLKLKEARLPLVIEKVC 709
 Query Match 21.4%; Score 523.5; DB 1; Length 790;
 Best Local Similarity 41.4%; Prod. No. 4.6e-34; Indels 21; Gaps 6;
 Matches 108; Conservative 43; Mismatches 89;
 Qy 370 NHDRVIGGIISPMSLCAGLTGVDSCQDGSGLVYCERRQRLKLKGATSGIGGCAEVNK 429
 Db 710 NRVEVIGKVSPLNELCAGHLAGGIDSCQSBGSGPFLVCPFKDVKYVLOQ3VTSWGIQCALPNK 769
 Query Match 21.4%; Score 523.5; DB 1; Length 790;
 Best Local Similarity 41.4%; Prod. No. 4.6e-34; Indels 21; Gaps 6;
 Matches 108; Conservative 43; Mismatches 89;
 Qy 430 PGVYTRVTSFLDWHQMERD 450
 Db 770 PGVYTRVTSFLDWHQMERD 790

A;Residues: 1-273 <MCN>
A;Cross-references: GB:U00653; NID:G200518; PID:AAA39992.1; PMID:9200519
A;Note: sequence extracted from NCBI backbone (NCBIN:119745; NCBI:P:119746)
C;Superfamily: trypsin, trypsin homology
C;Keywords: hydrolase; serine protease
R;19-265/Domain: trypsin homology <TRY>
Query Match Score 504; DB 2; Length 273;
Best Local Similarity 42.2%; Prod. No. 5e-33; Gaps 8;
Matches 105; Conservative 40; Mismatches 84; Indels 20; Gaps 8;
Qy 217 IVGGNSLISQWPQAISLFOQ --YHCGGSTIPWITAAHCV-YDLYLPKSTIQ 272
Db 29 IVGGQEAEHGNKWKPVQSLRANDTYWMHFGGSIHPQWVLTAAHCYGPDVADENPKVRL 88
Qy 273 GLVSILDNPAPSHI--VERKIVTHSKYKEPKRLNDIAALMKAQLPLTFENEMIQPCVLENSEE 330
Db 89 RKQLYHH--DHMTVSGQIITPDPFIVQDADIALKLKLTIPNVPNTSDYFVPLPRAE 145
Qy 331 NEFDGKVWTCWTSQMGATEDDGDAASP--VLNHAAYPLSNIKIN--HRDVYGG---LISP 381
Db 146 TFPSTGLCIVVQVGMNIDN:VNLPPPFKLEVQVPIENHLCDLKTKHGKLTGDNTEVRL 205
Qy 382 SMICAGYLITGGVNBSCQGDGGPLVQCEBRILKVGATSGFEGIGCAELNKPGYVYTRVSEFL 441
Db 206 DMLCAG--MEGHDSQCQGDGGPLVCKYDTWLOAQVVSWEGBCAQPNRPGTYTRVYLLD 263
Qy 442 WIHQMERD 450
Db 264 WIHYVVKD 272

A;Pathway: blood coagulation intrinsic pathway
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydrolysis; heavy chain
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-387/Product: coagulation factor XIa heavy chain #status experimental <LCX>
F;19-108/Domain: apple repeat <AP1>
F;109-198/Domain: apple repeat <AP2>
F;189-288/Domain: apple repeat <AP3>
F;388-625/Product: coagulation factor XIa light chain #status experimental <TRY>
F;388-618/Domain: trypsin homology <TRY>
F;103-514-581,571-599/Disulfide bonds: #status Predicted
F;29/Disulfide bonds: interchain #status experimental F:46-76 50-110-193 136-165 140-146-200-226-555-230-236-321-327, 38(F:90-126 353,450 Binding site: carbohydrate (Asn) (covalent) #status Predicted
F;33/Disulfide bonds: interchain #status predicted
F;387-388/Cleavage site: Argile (coagulation factor XIa) #status experimental
F:431-480 575/Active site: His ASP Ser #status predicted
F;491/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match Score 504; DB 1; Length 625;
Best Local Similarity 36.7%; Prod. No. 1.3e-32;
Matches 103; Conservative 44; Mismatches 103; Indels 16; Gaps 5;
Qy 193 GCASHVVTI-----QCPAGHRRGYSRIVGANMSLJUNPQASIQFOQG --YHLCGG 244
Db 364 GGISGYTIRLCKMDNECT----KIKRIVGTGEGWPKQVLTTSPTQRHLCGG 418
Qy 245 SVITPLWITTAACVYDYLPLPKSMWTLQVGLV- SLLDNPAPSHLVEKLYVHSKYKPKRLG 302
Db 419 SIIGNQWILITAACFCYGVESPKLRLRVGILNGSEIIKDTSFFGVOEIIHDYOKMAESG 478
Qy 303 NDIALMKLAGPLTNEMFQPVCLPNSENFPDGKVCWTSGWGRATEDDGDSAPYLNHAAP 362
Db 479 YDALLKLETTVNYTDQBPCILPSKGDRNVIYTDCWVQGWGYRKLRDKIONTLQKAKIP 538
Qy 363 LISNKCNCNRDVGYGIISISMCLAGYLTTGVDSSQGDSSGGLVQCEBRILKVGATSGI 422
Db 539 LVINNECQRR-YRGHKITHKMICGYREGKDACKGDSGGPLSCKHNNEWVHLVGTISWGE 597
Qy 423 GCAEVTKPGVYTRYTSFLDWTHEOME 448
Db 598 GCAQRERPGVYTNVVEYDWLRIQ 623

Search completed: May 5, 2004, 15:48:51
Job time : 21 secs

RESULT 15
KFMU
coagulation factor XIa (EC 3.4.21.27) precursor [validated] - human
N;Alternative names: antihemophilic factor C; plasma thromboplastin antecedent
C;Species: Homo sapiens (man)
C;Accession: A27431; A00920; A37140
R;Asakai, R.; Davie, E.W.; Chung, D.W.
Biochemistry 26, 7221-7228, 1987
A;Title: Organization of the gene for human factor XI.
A;Reference number: A27431; MUID:88107663; PMID:2827746
A;Accession: A27431
A;Molecule type: DNA
A;Residues: 1-625 <ASA>
A;Cross-references: GB: M18295
A;Note: the sequence shown follows the authors' translation
R;Fujiikawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.
Biochemistry 25, 2417-2424, 1986
A;Title: Amino acid sequence of human factor XI, a blood coagulation factor with four tandem repeats
A;Accession number: A00920; MUID:86243360; PMID:3636155
A;Accession: A00920
A;Molecule type: protein
A;Residues: 1-625 <PLJ>
A;Cross-references: GB: M13142; NID:gi192832; PID:AAA52487.1; PMID:9182833
R;McMullan, B.A.; Fujiikawa, K.; Davie, E.W.
Biochemistry 30, 2056-2060, 1991
A;Title: Location of the disulfide bonds in human coagulation factor XI: the presence of he active site, and a heavy chain, which associates with high molecular weight (HMW) kinins
C;Genetics:
A;Gene: GDB:F11
A;Cross-references: GDB:119891; OMIM:264900
A;Map position: 4q35-q35
A;Introns: 19-/; 73-/; 109-/; 162-/; 199-/; 252-/; 289-/; 343-/; 379-/; 435-/; 494-/; 52
C;Function:
A;Description: catalyzes the proteolytic activation of coagulation factor IX